

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 25, 2003, 14:47:45 ; Search time 2250 Seconds
(without alignments)
6240.661 Million cell updates/sec

Title: US-09-601-267-36

Perfect score: 867

Sequence: 1 agctactcagagagctgaga.....ccctaactgagaagggcgta 867

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues 32308132

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estbda:*
2: em_esthum:*
3: em_estln:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	110.8	12.8	466	17	AQ229478 HS.2021.A
2	109.2	12.6	680	17	AG186502 Pan. trogl
3	107.6	12.4	418	17	AQ390169 CITHI-El-
4	107.2	12.4	469	13	BM509394 Ih17F10.Y
5	107.2	12.4	516	13	BI468297 Id87B01.Y
6	107.2	12.4	529	14	BQ270800 IK05B06.Y

7	107.2	12.4	556	14	BQ267333	BQ267333	IK02C03.Y
8	107.2	12.4	589	14	BQ270346	BQ270346	IK09G10.Y
9	106.4	12.3	635	17	AQ428429	AQ428429	CITBI-El-
10	106	12.2	774	17	AQ751486	AQ751486	HS.5576.B
11	104.8	12.1	671	17	AQ418931	AQ418931	RPCT-11-1
12	104.6	12.1	465	17	AQ527107	AQ527107	CITBI-El-
13	104.4	12.0	815	14	BQ429052	BQ429052	AGENCOURT
14	104.4	12.0	303	14	BM672404	BM672404	UI-E-COO-
15	104.4	12.0	712	17	AG139751	AG139751	Pan. trogl
16	103.8	12.0	451	14	M66929	M66929	z447H09.S1
17	103	11.9	837	13	BI820230	BI820230	603037070
18	103	11.9	1074	14	BQ429712	BQ429712	AGENCOURT
19	102.8	11.9	318	13	BI492686	BI492686	dE27G08.W
20	102.8	11.9	340	10	AM021747	AM021747	dE27G08.Y
21	102.8	11.9	684	17	AG109444	AG109444	Pan. trogl
22	102	11.8	364	17	AQ333390	AQ333390	HS.5010.A
23	101.6	11.7	256	9	AA084337	AA084337	zn04D05.S
24	101.2	11.7	382	10	AV764523	AV764523	AV764523
25	101.2	11.7	474	9	AI866580	AI866580	lz51C10.X
26	101.2	11.7	514	17	B37536	B37536	HS-1044-A1-
27	101.2	11.7	735	9	AU120382	AU120382	AI120382
28	101.2	11.7	773	12	BG221771	BG221771	RST41586
29	101.2	11.7	815	12	BE382750	BE382750	601816513
30	101.2	11.7	859	17	AQ750588	AQ750588	HS.5573.B
31	101.2	11.7	925	12	BG249993	BG249993	602362061
32	101	11.6	445	17	AO198078	AO198078	RPCT11-46
33	100.4	11.6	504	9	AI138096	AI138096	DKFZP547B
34	100.2	11.6	335	9	AA492202	AA492202	ng78E08.S
35	100	11.5	459	17	AQ483064	AQ483064	RPCT-11-2
36	99.8	11.5	404	14	W07861	W07861	zb04G03.r1
37	99.8	11.5	460	9	AI597733	AI597733	tu91A08.X
38	99.8	11.5	464	10	AM150226	AM150226	xg49A01.X
39	99.8	11.5	662	17	AO262070	AO262070	CITBI-El-
40	99.8	11.5	712	9	AL709370	AL709370	DKFZP686K
41	99.6	11.5	238	17	AQ344289	AQ344289	RPCT11-12
42	99.6	11.5	281	9	AI453660	AI453660	cl28F08.X
43	99.6	11.5	419	17	AO303684	AO303684	CIT-HSP-2
44	99.6	11.5	494	12	BF916367	BF916367	IL3-UT011
45	99.6	11.5	1661	11	AY037152	AY037152	Homo sapi

ALIGNMENTS

RESULT 1
LOCUS AQ229478/c 466 bp DNA linear GSS 26-SEP-1998
DEFINITION HS_2021_A2_A08_MR CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=2021 COL=16 Row=A, DNA sequence.
ACCESSION AQ229478
VERSION AQ229478.1 GI:3654707
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 466)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,D., Zhao,S., Adams,M.D. and
Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 2021 row: A column: 16

Class: BAC ends
High quality sequence stop: 466.

FEATURES
Location/Qualifiers
1. 466

BASE COUNT 113 a 94 c 111 g 147 t 1 others
ORIGIN
Query Match 12.8%; Score 110.8; DB 17; Length 466;
Best Local Similarity 90.8%; Pred. No. 1.3e-18;
Matches 118; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 AGCTACTCAGGAGCGCTGAGACGAGAAATCGCTGAACCCGAGAGAGAGTTCAGTG 60
|||||
Db 399 AGCTACTCAGGAGCGCTGAGAGAGAAATCACTTGAACCCGAGAGCGAGTTGCACTG 340
QY 61 AGCCGAGATCAGCCGCTAGACTCCATCCAGCTGGCGGAAAGAGCAAGACTCCGCTCA 120
|||||
Db 339 AGCCAGATCAGCCGCTAGCTCATCCAGCATGAGAGAGCAAGCAAGACTCCGCTCA 280
QY 121 AAAAAAAAAA 130
|||||
Db 279 AAAAAAAAAA 270

RESULT 2
AG186502 680 bp DNA linear GSS 09-JAN-2002
LOCUS
DEFINITION Pan troglodytes DNA, clone: RP43-060015.T7, genomic survey
ACCESSION AG186502
VERSION AG186502.1 GI:16716182
KEYWORDS GSS.
SOURCE Pan troglodytes male lymphocytes DNA, clone_lib:RPCI-43 Chimpanzee
ORGANISM Male BAC library clone:RP43-060015.T7.

REFERENCE
AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoh.Y., Watanabe,H. and Sakaki,Y.
TITLE Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suenhiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimpesegsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT Clones are derived from the chimpanzee BAC library RPCI-43 This BAC
end was generated during the Rad process and may have higher chance
of clone tracking errors.
PRIMERS
Sequencing: T7

LIBRARY
Vector : pBACE3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI
Location/Qualifiers
1. 680
/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="RP43-060015.T7"
/sex="male"

FEATURES
source

BASE COUNT 194 a 156 c 163 g 121 t 46 others
ORIGIN
Query Match 12.6%; Score 109.2; DB 17; Length 680;
Best Local Similarity 87.0%; Pred. No. 3.5e-18;
Matches 120; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 1 AGCTACTCAGGAGCGCTGAGACGAGAAATCGCTGAACCCGAGAGAGAGTTCAGTG 60
|||||
Db 239 AGCTACTCAGGAGCGCTGAGAGAGAAATCGCTTGAACCTAGAGAGCGAGTTGCACTG 298
QY 61 AGCCGAGATCAGCCGCTAGACTCCATCCAGCTGGCGGAAAGAGCAAGACTCCGCTCA 120
|||||
Db 299 AGCCGAGATCAGCCGCTAGCTCATCCAGCTGCGGCGAGAGAGCAAGACTCCGCTCA 358
QY 121 AAAAAAAAAATCGTTACA 138
|||||
Db 359 AAAAAAAAAAAGAAAAA 376

RESULT 3
AQ390169 418 bp DNA linear GSS 06-MAR-1999
LOCUS
DEFINITION CITR1-EI-2544A19.TF CITR1-EI Homo sapiens genomic clone 2544A19,
DNA sequence.
ACCESSION AQ390169
VERSION AQ390169.1 GI:4361192
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 418)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
Venter,J.C.
TITLE Use of BAC End Sequences from Caltech Libraries for Sequence-Ready
Map Building (1997)
JOURNAL Unpublished (1997)
COMMENT Other_GSSs: CITR1-EI-2544A19.TF
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbeetlgr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/cdb/hunggen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.

FEATURES
source
1. 418
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2544A19"
/clone_lib="CITR1-EI"
/sex="male"
/cell_type="sperm"
/note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI;
Caltech Human BAC Library p"

BASE COUNT 132 a 109 c 104 g 73 t
ORIGIN
Query Match 12.4%; Score 107.6; DB 17; Length 418;
Best Local Similarity 86.2%; Pred. No. 8.9e-18;
Matches 119; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 1 AGCTACTCAGGAGCGCTGAGACGAGAAATCGCTGAACCCGAGAGAGAGTTCAGTG 60
|||||
Db 95 AGCTGCTCAGAGAGCGCTGAGAGCAATGGAATCACTTGAACCCGAGAGAGAGTTCAGTG 154

0y 61 AGCCGAGATCAGCCACTAGACTCCATCCAGCCTGGGCGAAAGACAGACTCCCTCTCA 120
|||||
Db 155 AGCCGAGATCAGCCACTAGACTCCATCCAGCCTGGGCGAAAGACAGACTCCCTCTCA 214
0y 121 AAAAAAAAAATCGTTTACA 138
|||||
Db 215 AAAAAAAAAAACAACA 232

RESULT 4
LOCUS

BM509394 469 bp mRNA linear EST 15-FEB-2002
1h7f10.y1 Human Insulinoma Homo sapiens cDNA 5' similar to
SW:ALU8.HUMAN.P39195.ALU.SUBFAMILY.SX.SEQUENCE.CONTAMINATION

WARNING ENTRY. [1] ; mRNA sequence.

BM509394.1 GI:18680537
EST.

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 469)
Melton,D., Brown,J., Kenty,G., Permult,A., Lee,C., Kaestner,K.,
Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritzer,E., Ronko,I., Bennett,J., Cardenas
, M., Gibbons,M., McCann,R., Cole,R., Tsagarelshvili,R., Williams,T.,
Jackson,Y. and Bowers,Y.

Endocrine Pancreas Consortium
Unpublished (2000)

CONTACT: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute

Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557

Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. J. Ferrer In vivo mass-excised to
pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington

University Genome Sequencing Center For information on obtaining a
clone please contact: Dr. Hiroshi Inoue (hinoue@wustl.edu)
Seq primer: -40RP from G1bco
High quality sequence stop: 416.

FEATURES

SOURCE

Location/Qualifiers

1..469

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="Human Insulinoma"

/tissue_type="Insulinoma"

/lab_host="DH10B (phage-resistant)"

/note="Organ: pancreas; Vector: pBluescript SK-; Site:1:
XhoI; Site:2: EcoRI; Constructed with lambda ZapII system
(Stratagene) by Dr. J. Ferrer. In vivo mass-excised to
pBluescript SK- by Dr. H. Inoue following the Washington

University protocol
(http://genome.wustl.edu/est/lambda-protocol.shtml).

Please contact Hiroshi Inoue, MD/PhD for further
information on this library (Metabolism Division, Permut
Laboratory, Washington University School of Medicine, Box
8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this
is a Washington University Pancreas EST project library."

BASE COUNT 149 a 93 c 94 g 133 t

ORIGIN

Query Match 12.4%; Score 107.2; DB 13; Length 469;
Best Local Similarity 81.6%; Pred. No. 1.1e-17;
Matches 124; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

0y 1 AGCTACTGAGGAGGCTGACAGCAATCGCTTGAAACCCGGAGGACGAGCTTGCACTG 60
|||||

Db 285 AGCCACTGGGAGGCTTAAATGGAGAAATCGCTTGAAACCTGGAGGCGAGAGCTTGCACTG 344
0y 61 AGCCGAGATCAGCCACTAGACTCCATCCAGCCTGGGCGAAAGACAGACTCCCTCTCA 120
|||||
Db 345 AGCCGAGATCAGCCACTAGACTCCATCCAGCCTGGGCGAAAGACAGACTCCCTCTCA 404
0y 121 AAAAAAAAAATCGTTTACA 152
|||||
Db 405 AAAAAAAAAAGTTAGAAAAATGCTCTTT 436

RESULT 5

LOCUS

BI468297 516 bp mRNA linear EST 11-MAR-2002
1d87b01.y1 Human Insulinoma Homo sapiens cDNA clone IMAGE:5022649

5', mRNA sequence.

BI468297.1 GI:15284406
EST.

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 516)
Melton,D., Brown,J., Kenty,G., Permult,A., Lee,C., Kaestner,K.,
Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritzer,E., Ronko,I., Bennett,J., Cardenas
, M., Gibbons,M., McCann,R., Cole,R., Tsagarelshvili,R., Williams,T.,
Jackson,Y. and Bowers,Y.

Endocrine Pancreas Consortium
Unpublished (2000)

CONTACT: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute

Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557

Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. J. Ferrer In vivo mass-excised to
pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington

University Genome Sequencing Center For information on obtaining a
clone please contact: Dr. Hiroshi Inoue (hinoue@wustl.edu)
High quality sequence stop: 457.

FEATURES

SOURCE

Location/Qualifiers

1..516

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="IMAGE:5022649"

/clone_lib="Human Insulinoma"

/tissue_type="Insulinoma"

/lab_host="DH10B (phage-resistant)"

/note="Organ: pancreas; Vector: pBluescript SK-; Site:1:
XhoI; Site:2: EcoRI; Constructed with lambda ZapII system
(Stratagene) by Dr. J. Ferrer. In vivo mass-excised to
pBluescript SK- by Dr. H. Inoue following the Washington

University protocol
(http://genome.wustl.edu/est/lambda-protocol.shtml).

Please contact Hiroshi Inoue, MD/PhD for further
information on this library (Metabolism Division, Permut
Laboratory, Washington University School of Medicine, Box
8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this
is a Washington University Pancreas EST project library."

BASE COUNT 157 a 103 c 104 g 152 t

ORIGIN

Query Match 12.4%; Score 107.2; DB 13; Length 516;
Best Local Similarity 81.6%; Pred. No. 1.2e-17;
Matches 124; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

0y 1 AGCTACTGAGGAGGCTGACAGCAATCGCTTGAAACCCGGAGGACGAGCTTGCACTG 60
|||||

Db 285 AGCCACTCGGAGGCTTAAATGGAGAAATCCGTTGAACCTTGAGAGCAGAGCTTGCAATG 344
QY 61 AGCGAGATCAGCGACATCCATCCAGCTGGGCGGAAGAGCAAGACTCCGTCICA 120
Db 345 AGCCAGAGCCAGCGACATCCATCCAGCTGGGCTGAGAGAGCAAGACTCATCTCA 404
QY 121 AAAAAAAAAATCGTTACATTTATGTCGATT 152
Db 405 AAAAAAAAAAGTTAGAAAAATGCTCTTT 436

RESULT 6
LOCUS BQ270800
DEFINITION BQ270800 529 bp mRNA linear EST 07-MAY-2002
1K05D06.Y1 Human Insulinoma Homo sapiens cDNA clone IMAGE: 5779930
5', mRNA sequence.
ACCESSION BQ270800
VERSION BQ270800.1 GI:20495866
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 529)
Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Rilter,E., Ronko,I., Bennett,J., Cardenas
,M., Gibbons,M., McCann,R., Cole,R., Tsagarashvilli,R., Williams,T.,
Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Other ESTs: 1K05D06.X1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. J. Ferrer In vivo mass-excised to
pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
University Genome Sequencing Center For information on obtaining a
clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
Seq primer: -40RP from Gibco
High quality sequence stop: 428.
Location/Qualifiers
1..529
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE: 5779930"
/clone_id="Human Insulinoma"
/tissue_type="Insulinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: pancreas; Vector: pBluescript SK-; Site:1:
XhoI; Site_2: EcoRI; Constructed with lambda ZapII system
pBluescript SK- by Dr. J. Ferrer. In vivo mass-excised to
pBluescript SK- by Dr. H. Inoue following the Washington
University protocol
(http://genome.wustl.edu/est/lambda_protocol.shtml).
Please contact Hiroshi Inoue, MD/PhD for further
information on this library (Metabolism Division, Permutt
Laboratory, Washington University School of Medicine, Box
8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this
is a Washington University Pancreas EST project library."

BASE COUNT 160 a 107 c 107 g 155 t
ORIGIN

Query Match 12.4%; Score 107.2; DB 14; Length 529;
Best Local Similarity 81.6%; Pred. No. 1.2e-17;
Matches 124; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 1 AGTACTCAGAGGCTGAGACAGAGAAATCGTTGAACCCGAGAGCAGAGCTTGCAATG 60
Db 285 AGCCACTCGGAGGCTTAAATGGAGAAATCCGTTGAACCTTGAGAGCAGAGCTTGCAATG 344
QY 61 AGCGAGATCAGCGACATCCATCCAGCTGGGCGGAAGAGCAAGACTCCGTCICA 120
Db 345 AGCCAGAGCCAGCGACATCCATCCAGCTGGGCTGAGAGAGCAAGACTCATCTCA 404
QY 121 AAAAAAAAAATCGTTACATTTATGTCGATT 152
Db 405 AAAAAAAAAAGTTAGAAAAATGCTCTTT 436

RESULT 7
LOCUS BQ267333
DEFINITION BQ267333 556 bp mRNA linear EST 07-MAY-2002
1K02C03.Y1 Human Insulinoma Homo sapiens cDNA clone IMAGE: 5779589
5', mRNA sequence.
ACCESSION BQ267333
VERSION BQ267333.1 GI:20492398
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 556)
Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Rilter,E., Ronko,I., Bennett,J., Cardenas
,M., Gibbons,M., McCann,R., Cole,R., Tsagarashvilli,R., Williams,T.,
Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. J. Ferrer In vivo mass-excised to
pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
University Genome Sequencing Center For information on obtaining a
clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
Seq primer: -40RP from Gibco
High quality sequence stop: 428.
Location/Qualifiers
1..556
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE: 5779589"
/clone_id="Human Insulinoma"
/tissue_type="Insulinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: pancreas; Vector: pBluescript SK-; Site:1:
XhoI; Site_2: EcoRI; Constructed with lambda ZapII system
pBluescript SK- by Dr. J. Ferrer. In vivo mass-excised to
pBluescript SK- by Dr. H. Inoue following the Washington
University protocol
(http://genome.wustl.edu/est/lambda_protocol.shtml).
Please contact Hiroshi Inoue, MD/PhD for further
information on this library (Metabolism Division, Permutt
Laboratory, Washington University School of Medicine, Box
8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this
is a Washington University Pancreas EST project library."

BASE COUNT 167 a 112 c 113 g 164 t
ORIGIN

Query Match 12.4%; Score 107.2; DB 14; Length 556;
Best Local Similarity 81.6%; Pred. No. 1.2e-17;
Matches 124; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

[illegible]

Matches	124:	Conservative	0:	Mismatches	28:	Indels	0:	Gaps	0:
QY	1	AGCTACTCAGACGGCTGAGACACGAGATCCGCTTGAACCCGGGAGCGAGCTTGCAATG	60						
Db	285	AGCCACTCGGAGGCTTAAATGAGAAATCCCTTGAACCCGAGGAGGAGCTTGCAATG	344						
QY	61	AGCCGAGATCAGCGCAGCTAGACTCCATCCACCTCGGGCGGAAGAAGCAAGACTCCGCTCA	120						
Db	345	AGCCAGAGACCCAGCCACTGCCTCATTCACCTCGGGTGGAGACAGCAAGACTCCATCTCA	404						
QY	121	AAAAAAAAAATCGTTACAAATTATGTGGAAAT	152						
Db	405	AAAAAAAAAAAAAGTTAGAAAAATCGTCCTT	436						
RESULT 9	AO428429	635 bp	DNA	linear	GSS 24-MAR-1999				
LOCUS	AO428429								
DEFINITION	CITBI-El-2564J3.TF CITBI-El Homo sapiens genomic clone 2564J3, DNA sequence.								
ACCESSION	AO428429								
VERSION	AO428429.1								
KEYWORDS	GSS.								
SOURCE	human.								
ORGANISM	Homo sapiens								
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.								
AUTHORS	1 (bases 1 to 635) Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and Venter,J.C.								
TITLE	Use of BAC End Sequences from CalTech Libraries for Sequence-Ready Map Building								
JOURNAL	Unpublished (1997)								
COMMENT	Other_GSSs: CITBI-El-2564J3.TR Contact: Shaying Zhao, William Nierman, Mark Adams Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850 Tel: 301 838 0200 Fax: 301 838 0208 Email: jhbe@tigr.org Clones are available from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html. Seq primer: M13-21 Class: BAC ends.								
FEATURES	location/Qualifiers								
SOURCE	1..635								
	/organism="Homo sapiens"								
	/db_xref="taxon:9606"								
	/clone="2564J3"								
	/clone_lib="CITBI-El"								
	/sex="male"								
	/cell_type="sperm"								
	/note="Vector: pBelobAC11, Site_1: EcoRI; Site_2: EcoRI; Caltech Human BAC Library D"								
BASE COUNT	218 a 129 c 119 g 169 t								
ORIGIN									
Query Match	12.38;	Score 106.4;	DB 17;	Length 635;					
Best Local Similarity	67.38;	Pred. No. 1.9e-17;							
Matches 167; Conservative	0;	Mismatches 76;	Indels 5;	Gaps 1;					
QY	1	AGCTACTCAGACGGCTGAGACACGAGATCCGCTTGAACCCGGGAGCGAGCTTGCAATG	60						
Db	307	AGCTATTCAGAGACCTTAGGACGAGAGATTCCTTGAACCCGGGAGGTGGAGATTCACATG	366						
QY	61	AGCCGAGATCAGCGCAGCTAGACTCCATCCACCTCGGGCGGAAGAAGCAAGACTCCGCTCA	120						
Db	367	AGCCGAGATCCCGGACAGCTGCATTCACCTCGGGCGGAGAGAGTAGATCCACGCTCA	426						
QY	121	AAAAAAAAAATCGTTACAAAT-----TTATGTGGATTAATCTCCCTCTTTTAACTCATCA	175						

Db	427	AAAAAAAAAAAAAAAAAATTCACCTTTAAACGTATACCTACACCCAGTTCATCAGACAA	486
Oy	176	AGACACAGCAGCAGCTTTTAAAGCAAGTCATGATTTGAAACGCCCTTTCTTCTAATAAA	235
Db	487	ACTACACAGGAGATACAGATTAACCTTAATTATGATTTACCAAGATTAATTTGATAATAA	546
Oy	236	GGGAGATT 243	
Db	547	TAGACAGT 554	
RESULT 10			
LOCUS	AO751486		
DEFINITION	AO751486	774 bp	DNA
	HS-5576-B2-B05-SP6 RPC1-11 Human Male BAC Library Homo sapiens		linear GSS 19-JUL-1999
ACCESSION	AO751486		genomic clone Plate-1152 Col-10 Row-D, DNA sequence.
VERSION	AO751486.1	GI:5538644	
KEYWORDS	GSS.		
SOURCE	human.		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 774)		
AUTHORS	Mahairas G.G., Wallace, J.C., Smith, R., Swartzell, S., Holzman, T.,		
	Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and		
	Hood, L.		
TITLE	Sequence-tagged connectors: A sequence approach to mapping and		
	scanning the human genome		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)		
COMMENT	99380589		
	Contact: Mahairas GG, Wallace JC, Hood L		

High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel.: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library Rpci-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPac Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Research Genetics (inforesgen.com). BAC end Web Server: <http://www.htsc.washington.edu>
Plate: 1152 row: D column: 10
Seq primer: SP6
Class: BAC ends
High quality sequence stop: 774.

FEATURES	source	Location/Qualifiers
	1. .774	/organism="Homo sapiens" /db_xref="taxon:3606" /clone_plate=152 Col=10 Row=D" /clone_id="RPC1-11 Human Male BAC Library" /sex="male" /note="Vector: pBACe3.6; Site.1: EcoRI; Site.2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI-Methylase. Site selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"
BASE COUNT	258 a	192 c 177 g 143 t 4 others
ORIGIN		

	Query Match	12.2%	Score 106;	DB 17;	Length 774;
	Best Local Similarity	88.5%;	Pred. No. 2.5e-17;		
	Matches 115; Conservative	0;	Mismatches 15;	Indels 0;	Gaps 0;
QY	1 AGCTACTAGGAGCGCTGTAGACACAGCATCCGTTGAACCCGGGAGGCAGAGTTCGCAATG	60			
Dd	248 AGCTACTAGGAGCGCTGTAGAGCAGGAATGGCATGTAACCTCGGAAATCAGAGCTTCGCAATG	307			
QY	61 AGCCGAGATCACGCCACTAGACTCCATCCAGGCTTGCGGGAAGAAGACAGACTTCGCTTCCA	120			

Db	308	AGCCAAAGATCTTCGCGACCTGCACACTGCATTCGACGCTTGCGGAGACAGAGCACTGTCTCA	367
OY	121	AAAAAAAAAAAA 130 	
Db	368	AAAAAAAAAAAA 377	
RESULT 11			
LOCUS	AQ418931		
DEFINITION	AQ418931	671 bp	DNA
	RPCT-11-179H11.TV	RPCT-11 Homo sapiens	genomic clone RPCT-11-179H11
ACCESSION	RPCT-11-179H11		
VERSION	AQ418931		
KEYWORDS	AQ418931.1	GI:4476655	
SOURCE	GSS.		
ORGANISM	human.		
	Homo sapiens		
	EnxayrOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 671)		
REFERENCE	Zhuo, S., Adams, M.D., Niernan, W., Malek, J., de Jong, P. and Venter J.C		
AUTHORS			
TITLE	Use of Bac End Sequences from Library RPCT-11 for Sequence-Ready Map Building		
JOURNAL	Unpublished (1997)		
COMMENT	other_GSSs: RPCT-11-179H11.TV		

Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbeetlgr.org
Clones are derived from the human BAC library RPCR-11. For BAC library availability, please contact Pieter de Jong (pieter@ejl.jong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from Research Genetics (<http://resgen.com>). BAC end search page: http://www.tlgr.org/tldb/humang/bac_end_search/bac_end_search.html.
Seq primer: T7
Class: BAC ends.

FEATURES	SOURCE
location/Qualifiers	1. 671
/organism="Homo sapiens"	
/db_xref="GDB:7568530"	
/db_xref="taxon:9606"	
/clone="RPC1-11-179H11"	
/clone_lib="RPC1-11"	
/sex="Male"	
/cell_type="Lymphocytes"	
/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI; RPC111 Human Male BAC library"	
237 a	166 c 155 g 113 t

	Query Match	12.1%	Score 104.8	DB 17	Length 671	
	Best Local Similarity	84.3%	Pred. No. 5.1e-17			
	Matches 118:	Conservative	0	Mismatches 22	Indels 0	Gaps 0
QY	1 AGCTACTCAGGAGGGCTGTGACACGAAATCGCTTGAACCCGCGAGGCAGAGTTGCATGTG	60				
Db	248 AGCTACTCAAGAGGCTGTAGCGAGAGAATTCGACATGAACTCGGATGCGAGACTTGCAATG	307				
QY	61 AGCCGAGATCACGCCACATCTAGACTCCATCCACGCTTGCGGGAAGACGACAAGACTCCGTCTCA	120				
Db	308 AGCCGAGATCTCGGCCACATCGACTCCATCCACGCTTGCGGGAAGACGACAAGACTCCGTCTCA	367				
QY	121 AAAAAAAAAATCGTTACAAT	140				
Db	368 AAAAAAAAAAAAAACAATAAT	387				
	RESULT 12					

A0527107 465 bp DNA linear GSS 18-MAY-1999
LOCUS CITBI-E1-2603D20.TR CITBI-E1 Homo sapiens genomic clone 2603D20,
DEFINITION DNA sequence.
ACCESSION A0527107.1 GI:4838867
VERSION A0527107.1
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 465)
AUTHORS Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
Venter,J.C.
TITLE Use of BAC End Sequences from Caltech Libraries for Sequence-Ready
Map Building
JOURNAL Unpublished (1997)
COMMENT Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hoeftlgr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tldb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13 Reverse
Class: BAC ends.
FEATURES
source 1. .465
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2603D20"
/clone_lib="CITBI-E1"
/sex="male"
/cell_type="sperm"
/note="Vector: pBelobAC11; Site_1: EcoRI; Site_2: EcoRI;
Caltech Human BAC Library D"

BASE COUNT 157 a 102 c 109 g 97 t
ORIGIN

Query Match 12.1%; Score 104.6; DB 17; Length 465;
Best Local Similarity 78.6%; Pred. No. 5.6e-17;
Matches 125; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

OY 1 AGCTACTCAGGAGGCTGAGACACGAGAAATCGCTGAACCCGGGAGCAGAGTTCAGTG 60
|||||
DB 276 AGCTACTCAGGAGGCTGAGGCGAGAGAAATCGCTGAACCCAGAGGAGCAGTTCAGTG 335
|||||
OY 61 AGCCGAGATCAGCGCAGTACATCCATCCAGCTGGGGGAAAGACGACGATCCGCTCA 120
|||||
DB 336 AGTTAGATCAGACACGCTACTCACTCCAGGCTGTGTACGAGATGAGACTCCATCTCC 395
|||||
OY 121 AAAAAAATCGTTACAATTATGTTGATGATCTACCTCC 159
|||||
DB 396 AAAAAAAAAAAAAAAAAAACTTATGATATACCTAACC 434
|||||

RESULT 13
LOCUS BQ429052 815 bp mRNA linear EST 24-MAY-2002
DEFINITION AGENCOURT_7908333 NIH_MGC_82 Homo sapiens CDNA clone IMAGE:6102430
5', mRNA sequence.
ACCESSION BQ429052
VERSION BQ429052.1 GI:21168128
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 815)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: gcapsb-remail.nih.gov
Tissue Procurement: CLONTECH
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.lnl.gov
Plate: LICM237 row: a column: 23
High quality sequence stop: 479.
FEATURES
source 1. .815
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6102430"
/clone_lib="NIH_MGC_82"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: testis; Vector: pDNR-LIB (Clontech); Site 1:
SfiI (ggcgccctggcc); Site 2: SfiI (ggccatattggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATTATGACC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGCCGAGCGCCGACATG-dr(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size
1.35 kb (range 0.9-4.0 kb). 14/15 colonies contained
inserts by PCR. This library was enriched for full-length
clones and was constructed by Clontech Laboratories (Palo
Alto, CA)."

BASE COUNT 241 a 188 c 178 g 208 t
ORIGIN

Query Match 12.1%; Score 104.6; DB 14; Length 815;
Best Local Similarity 83.2%; Pred. No. 5.9e-17;
Matches 119; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

OY 1 AGCTACTCAGGAGGCTGAGACACGAGAAATCGCTTAACCCGGGAGCAGAGTTCAGTG 60
|||||
DB 163 AGCTACTCGGGGGGCTGAGGCGAGGAAATCGCTTAACCCGGGAGAGAGTTCAGTG 222
|||||
OY 61 AGCCGAGATCAGCGCAGTACATCCATCCAGCTGGGGGAAAGACGACGATCCGCTCA 120
|||||
DB 223 AGCCAAAGCTGGCGCAGTCACTCCAGCCAGCTGGGGGAGCAGACGAGTCCGCTCG 282
|||||
OY 121 AAAAAAATCGTTACAATTTA 143
|||||
DB 283 AAAAAAAAAAAAAAAAAAAGTGA 305
|||||

RESULT 14
LOCUS BM672404/c 303 bp mRNA linear EST 27-FEB-2002
DEFINITION UI-E-C00-adm-b-04-0-UI.s1 UI-E-C00 Homo sapiens CDNA clone
UI-E-C00-adm-b-04-0-UI 3', mRNA sequence.
ACCESSION BM672404
VERSION BM672404.1 GI:18982302
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 303)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250

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OM nucleic - nucleic search, using sw model

Run on: January 25, 2003, 13:39:25 : Search time 76 seconds
(without alignments)
3498.536 Million cell updates/sec

Title: US-09-601-267-36

Perfect score: 867
Sequence: 1 agctactcagagagctgaga.....ccctaactgagaagggcgta 867

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /cgn2_6/prodata/2/1na/5B_COMB.seq:*
3: /cgn2_6/prodata/2/1na/5A_COMB.seq:*
4: /cgn2_6/prodata/2/1na/5B_COMB.seq:*
5: /cgn2_6/prodata/2/1na/PCTUS_COMB.seq:*
6: /cgn2_6/prodata/2/1na/backfillseq1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	848.6	97.9	2420	1	US-08-330-123A-3	Sequence 3, Appl1
2	848.6	97.9	2420	4	US-09-380-517-3	Sequence 3, Appl1
3	848.6	97.9	2426	1	US-08-482-115B-3	Sequence 3, Appl1
4	848.6	97.9	2426	2	US-08-660-678A-3	Sequence 3, Appl1
5	848.6	97.9	2426	2	US-08-472-802C-4	Sequence 4, Appl1
6	848.6	97.9	2426	3	US-08-998-443-3	Sequence 1, Appl1
7	848.6	97.9	2426	4	US-09-060-523-3	Sequence 3, Appl1
8	848.6	97.9	2426	4	US-08-485-778-1	Sequence 1, Appl1
9	834.6	96.3	2425	3	US-08-520-550A-1	Sequence 1, Appl1
10	834.6	96.3	2425	3	US-08-714-482-2	Sequence 2, Appl1
11	334	38.4	981	2	US-08-710-249-5	Sequence 5, Appl1
12	333	38.4	981	4	US-09-220-157A-5	Sequence 2, Appl1
13	333	38.4	981	2	US-08-770-565-1	Sequence 1, Appl1
14	332.4	38.3	981	2	US-08-833-377-1	Sequence 1, Appl1
15	332.4	38.3	981	2	US-08-838-545-22	Sequence 22, Appl1
16	332.4	38.3	981	4	US-09-349-532-22	Sequence 22, Appl1
17	332.4	38.3	981	4	US-09-851-896-3	Sequence 22, Appl1
18	99.4	11.5	70000	4	US-08-324-465-2	Sequence 2, Appl1
19	97.6	11.3	1656	1	US-08-465-981-2	Sequence 2, Appl1
20	97.6	11.3	1656	5	PCT-US93-11915-2	Sequence 2, Appl1
21	97.6	11.3	1725	1	US-08-324-465-5	Sequence 5, Appl1
22	97.6	11.3	1725	5	PCT-US93-11915-5	Sequence 5, Appl1
23	97.6	11.3	1725	5	US-09-078-294-7	Sequence 7, Appl1
24	97.4	11.2	11811	4	US-09-078-294-9	Sequence 9, Appl1
25	96.4	11.1	1701	4	US-09-798-096-10	Sequence 10, Appl1
26	96.4	11.1	99500	4		
27	96	11.1				

C 28	95.6	11.0	14636	4	US-09-173-914-6	Sequence 6, Appl1
C 29	95.4	11.0	36159	4	US-09-749-588-3	Sequence 3, Appl1
C 30	95	11.0	9837	1	US-08-832-883-68	Sequence 68, Appl1
C 31	95	11.0	9837	2	US-08-832-877-68	Sequence 68, Appl1
C 32	94.8	10.9	176373	3	US-09-128-155-17	Sequence 17, Appl1
C 33	94.4	10.9	955	4	US-09-641-638-4	Sequence 4, Appl1
C 34	94.4	10.9	955	4	US-09-641-638-5	Sequence 5, Appl1
C 35	94.4	10.9	955	4	US-09-641-638-6	Sequence 6, Appl1
C 36	94.4	10.9	955	4	US-09-641-638-7	Sequence 7, Appl1
C 37	94.4	10.9	1000	4	US-09-641-638-650	Sequence 650, Appl1
C 38	94.4	10.9	3609	4	US-09-705-299-11	Sequence 11, Appl1
C 39	94.4	10.9	3844	4	US-09-689-423-1	Sequence 1, Appl1
C 40	94.4	10.9	246240	2	US-08-724-394A-20	Sequence 20, Appl1
C 41	94.4	10.9	246240	2	US-08-724-394A-21	Sequence 21, Appl1
C 42	94.4	10.9	246240	2	US-08-724-394A-22	Sequence 22, Appl1
C 43	94	10.8	866	4	US-09-257-179-11	Sequence 11, Appl1
C 44	94	10.8	2387	4	US-09-375-318-38	Sequence 38, Appl1
C 45	94	10.8	112132	4	US-09-741-150-3	Sequence 3, Appl1

ALIGNMENTS

RESULT 1
US-08-330-123A-3
Sequence 3, Application US/08330123A
Patent No. 5583016
GENERAL INFORMATION:
APPLICANT: VILLEPONTREAU, Bryant
APPLICANT: FENG, Junli
APPLICANT: FUNK, Walter
APPLICANT: ANDREWS, William H.
TITLE OF INVENTION: HUMAN TELOMERASE
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend Kourile and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/330,123A
FILING DATE: 27-OCT-1994
CLASSIFICATION: A35
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15389-000810
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2420 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-330-123A-3
Query Match 97.9%; Score 848.6; DB 1; Length 2420;
Best Local Similarity 99.4%; Pred. No. 1.2e-263;
Matches 862; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

Db 1141 AATCTTCTGTGAATTCATTTTAAAGTAGTCAGAGTGACACCGGCTGTCTGCAGA 1200
QY 541 GGATAGAAAAAGCCCTGTATACGTCAGTATAGTTTCACTTTAAAGAGGTGGGAAG 600
Db 1201 GGATAGAAAAAGCCCTGTATACGTCAGTATAGTTTCACTTTAAAGAGGTGGGAAG 1260
QY 601 TAAAGACGAACCCCTTTCGCGACGTGCGGAAGGCAACGTCCTTCATGAGCGGAA 660
Db 1261 TAAAGACGAACCCCTTTCGCGACGTGCGGAAGGCAACGTCCTTCATGAGCGGAA 1320
QY 661 ATGGAATTTAATTTCCGCTTCCCGCCACACAGCCCGCCGAGAGTAGTACTACAGAG 720
Db 1321 ATGGAATTTAATTTCCGCTTCCCGCCACACAGCCCGCCGAGAGTAGTACTACAGAG 1380
QY 721 AGCCGGAGAGTAGTACTACAGAGTAGTACTACAGAGTAGTACTACAGAGTAGTACTACAGAG 780
Db 1381 AGCCGGAGAGTAGTACTACAGAGTAGTACTACAGAGTAGTACTACAGAGTAGTACTACAGAG 1440
QY 781 CTCGCCCGGAGCGACACCGGTTGCGGAGGGTGGGCTGGAGGGGTGTCGCAATTTT 840
Db 1441 CTCGCCCGGAGCGACACCGGTTGCGGAGGGTGGGCTGGAGGGGTGTCGCAATTTT 1500
QY 841 TGTCTAACCTTAAGTGAAGAGGCGTA 867
Db 1501 TGTCTAACCTTAAGTGAAGAGGCGTA 1527

RESULT 3
US-08-482-115B-3
; Sequence 3, Application US/08482115B
; Patent No. 5776679
; General Information:
; APPLICANT: Villepeleau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Assays for the RNA Component of Human
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,115B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-00083005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2426 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-482-115B-3

Query Match 97.9%; Score 848.6; DB 1; Length 2426;
Best Local Similarity 99.4%; Pred. No. 1.2e-263;
Matches 862; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 AGCTACTCAGAGAGGCTGAGACACAGAGAAATCGCTTGAACCCGGAGGACAGAGTTCAGAG 60
Db 662 AGCTACTCAGAGAGGCTGAGACACAGAGAAATCGCTTGAACCCGGAGGACAGAGTTCAGAG 720
QY 61 AGCCGAGATCACCCCTAGACTATCCATCCAGCTGGGCGAAAGCAAGACTCCGCTCA 120
Db 721 AGCCGAGATCACCCCTAGACTATCCATCCAGCTGGGCGAAAGCAAGACTCCGCTCA 780
QY 121 AAAAAAAAAATCGTACAAATTTATGTTGATTAATCTCCCTCTTTTAACTCATCAAGACA 180
Db 781 AAAAAAAAAATCGTACAAATTTATGTTGATTAATCTCCCTCTTTTAACTCATCAAGACA 840
QY 181 CAGCAGTACTTTAAGCAAGATGATTTGAAGCGCTTTCTTCTCTAATAAAGGAG 240
Db 841 CAGCAGTACTTTAAGCAAGATGATTTGAAGCGCTTTCTTCTCTAATAAAGGAG 900
QY 241 ATTCAGTCTTAAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
Db 901 ATTCAGTCTTAAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
QY 301 AGGAGAGCTGAGAGAGGCAATTTCTAAGGAAAAAGGGCAAGGTTGGACATCGAGCAGATC 360
Db 961 AGGAGAGCTGAGAGAGGCAATTTCTAAGGAAAAAGGGCAAGGTTGGACATCGAGCAGATC 1020
QY 361 CCACAGAGCGGAGACAAAGATTTGCTGCTGATGATGATGATGATGATGATGATGATGATGAT 420
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Db 1081 AGTTTCACAAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
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Db 1141 AATCTTCTGTGAATTCATTTTAAAGTAGTCAGAGTGACACCGGCTGTCTGCAGA 1200
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Db 1501 TGTCTAACCTTAAGTGAAGAGGCGTA 1527

RESULT 4
US-08-660-678A-3
; Sequence 3, Application US/08660678A
; Patent No. 5837857

GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,678A
FILING DATE: 05-JUN-1996
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-000811US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ. ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2426 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-660-678A-3

Query Match 97.9%; Score 848.6; DB 2; Length 2426;
Best local Similarity 99.4%; Pred. No. 1.2e-263;
Matches 862; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 AGCTACTCAGAGGCTGAGACGACGAGANTCGTTGAACCCGGGAGCGACAGGTTGAGTG 60
DB 662 AGCTACTCAGAGGCTGAGACGACGAGANTCGTTGAACCCGGGAGCGACAGGTTGAGTG 720
QY 61 AGCCGAGATCAGCGCACTGACATCCATCCGCTGGCGGAAAGAGAGAGCTCCGTCTCA 120
DB 721 AGCCGAGATCAGCGCACTGACATCCATCCGCTGGCGGAAAGAGAGAGCTCCGTCTCA 780
QY 121 AAAAAAAAAAATCTTACATTTATGTTGATGTTACTCCCTCTTTTAACTCATCAGACA 180
DB 781 AAAAAAAAAAATCTTACATTTATGTTGATGTTACTCCCTCTTTTAACTCATCAGACA 840
QY 181 CAGCAGTACTTTAAGCAAAAGTCAATGATTGAAGCCCTTTCTTCTAATAAAGGAG 240
DB 841 CAGCAGTACTTTAAGCAAAAGTCAATGATTGAAGCCCTTTCTTCTAATAAAGGAG 900
QY 241 ATTCAGTCTTAAAGTAAATGATGATGTTACCTTGAATTAAGCCATCCTCTCTCA 300
DB 901 ATTCAGTCTTAAAGTAAATGATGATGTTACCTTGAATTAAGCCATCCTCTCTCTCA 960
QY 301 AGGAGAGCTGAGAGGATTTCTAAGGAAAAAGGGGAGGTTGAGACGCGGAGCATC 360
DB 961 AGGAGAGCTGAGAGGATTTCTAAGGAAAAAGGGGAGGTTGAGACGCGGAGCATC 1020

QY 361 CCACTGAGCCGAGACAAAGATTCTGCTAGTACGTGCTGCTGGAAATCATTTTCACA 420
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DB 1141 AATCTCTCTGTAATTTCCATTTTAAAGTAGTCGAGTGAACGCGCTGTGCTCACA 1200
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QY 601 TAAAGACGCAAGCCCTTCCCGGAGCTGGGAGAGGCAACGTCCTTCATGCGCGAA 660
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QY 661 ATGGAATTTAATTTCCGTTCCCGCCCAACGAGCCGCGGAGAGTAGTCTCAGAG 720
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QY 721 AGCCGAGAGTCAAGCTTGAGCAATCCGTGCGGTGCGGCGGCTCTTATTAAGCCGA 780
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QY 841 TGCTAACCTTAAGTGAAGGCGCTA 867
DB 1501 TGCTAACCTTAAGTGAAGGCGCTA 1527

RESULT 5
US-08-472-802C-4
Sequence 4, Application US/08472802C
Patent No. 5958680
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,802C
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15389-000820


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Db 781 AAAAAAAAAATGTTACAAATTAATGTTGATTAATCCCTCTTTTACCCTATCAAGACA 840
Qy 181 CAGACACTACTTTAAAGCAAGTCAATGTTAAAGCCCTTTCTTTCTTAATAAAGGAG 240
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Qy 241 ATTGAGTCCCTTAAGATTAATTAATGAGTATTAAGTATTAAGCAATCCCTGCTCA 300
Db 901 ATTGAGTCCCTTAAGATTAATTAATGAGTATTAAGTATTAAGCAATCCCTGCTCA 960
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Db 1441 CTCGCCCGGAGCGACCGGCTTCGCGAGAGGTGGCCTGGAGGGGTGGCCATTTT 1500
Qy 841 TGCTTAACCTTAAGTGAAGGCGCTA 867
Db 1501 TGCTTAACCTTAAGTGAAGGCGCTA 1527

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RESULT 7 US-08-998-443-3

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; Sequence 3, Application US/08998443
; Patent No. 6054575
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor

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; City: San Francisco
; State: California
; Country: USA
; Zip: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/998,443
; FILING DATE:
; CLASSIFICATION:
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,678
; FILING DATE: 05-JUN-1996
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000811US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
;
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2426 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
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; US-08-998-443-3

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Query Match          97.9%  Score 848.6; DB 3: Length 2426;
Best Local Similarity 99.4%  Pred. No. 1,2e-263;
Matches 862; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

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Qy 1 AGTACTCAGGAGGCTGAGACAGCAAGTCCGTTGAACCCGGGAGGACAGGTTGCAGTG 60
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Db 901 ATTGAGTCCCTTAAGATTAATTAATGAGTATTAAGTATTAAGCAATCCCTGCTCA 960
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Db 961 AGSAGAGCTGGAGAGGCAATTTCTAAGSAGAGAGGGGAGGTTGAACTCGAGCGATC 1020
Qy 361 CCATGAGAGCCGAGACAGATTTCTCTAGTCACTGCTGCTGGGAATCTATTTTCACAA 420
Db 1021 CCATGAGAGCCGAGACAGATTTCTCTAGTCACTGCTGCTGGGAATCTATTTTCACAA 1080
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Db 1081 AGTTCTCCAAAAATGTGATGATCAAAAGTAATGATGTTGTTGTTGTTAGGCCCTA 1140

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Db 1501 TGTCTAACCTTAACCTGAGAAAGGCGCTA 1527

RESULT 8
US-09-060-523-3
: Sequence 3, Application US/09060523
: Patent No. 6258535
: GENERAL INFORMATION:
: APPLICANT: Villeponteau, Bryant
: APPLICANT: Feng, Junli
: APPLICANT: Funk, Walter
: APPLICANT: Andrews, William H.
: TITLE OF INVENTION: Mammalian Telomerase
: NUMBER OF SEQUENCES: 25
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend and Crew LLP
: STREET: Two Embarcadero Center, Eighth Floor
: CITY: San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94111-3834
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/060,523
: FILING DATE: 14-APR-1998
: CLASSIFICATION: 536
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/660,678
: FILING DATE: 05-JUN-1996
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/330,123
: FILING DATE: 27-OCT-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/272,102
: FILING DATE: 07-JUL-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Storella, John R.
: REGISTRATION NUMBER: 32,944
: REFERENCE/DOCKET NUMBER: 015389-000813US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 576-0200
: TELEFAX: (415) 576-0300
: INFORMATION FOR SEQ ID NO: 3:

: SEQUENCE CHARACTERISTICS:
: LENGTH: 2426 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: US-09-060-523-3

Query Match 97.9%; Score 848.6; DB 4; Length 2426;
Best Local Similarity 99.4%; Pred. No. 1.2e-263;
Matches 862; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 AGCTACTCAGAGAGGCTGAGACAGAGAAATCGTTGAACCGGAGGACAGAGTTGAGATG 60
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Db 662 AGCTACTCAGAGAGGCTGAGACAGAGAAATCGTTGAACCGGAGGACAGAGTTGAGATG 720
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Db 781 AAAAAAATCGTTCAATTTATGATGATTAATCTCCCTTTTAAACCTATCAACAGCA 840
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Db 841 CACCACTACTTTTAAAGCAAAATGATTAAGAAAGCCCTTTCTTCTTAATAAAGGAG 900
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QY 1321 ATGGAACCTTAATTTCCCGTTCCCGCCCAACCAAGCCGCGGAGAGTAGTCACTCAGAG 720
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Db 721 ATGGAACCTTAATTTCCCGTTCCCGCCCAACCAAGCCGCGGAGAGTAGTCACTCAGAG 780
QY 781 AGCCGGAGAGTCAAGCTTGGCCCAATCCGTGCGGTGCGGCGCCGCTCCCTTTATAAGCCGA 1440
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Db 1441 AGCCGGAGAGTCAAGCTTGGCCCAATCCGTGCGGTGCGGCGCCGCTCCCTTTATAAGCCGA 1500
QY 841 TGTCTAACCTTAACCTGAGAAAGGCGCTA 867
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Db 1501 TGTCTAACCTTAACCTGAGAAAGGCGCTA 1527

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      9 RESULT 9
US-08-485-778-1
; Sequence 1, Application US/08485778
; Patent No. 5876979
; GENERAL INFORMATION:
; APPLICANT : Andrews, William H.
; APPLICANT : Avilion, Ariel Athena
; APPLICANT : Feng, Junli
; APPLICANT : Funk, Walter
; APPLICANT : Greider, Carol
; APPLICANT : Maruhenda, Maria Antonia Blasco
; APPLICANT : Villeponteau, Bryant
; TITLE OF INVENTION : RNA COMPONENT OF TELOMERASE
; NUMBER OF SEQUENCES : 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET : Two Millita Drive
; CITY : Lexington
; STATE : MA
; COUNTRY : US
; ZIP : 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER : IBM PC compatible
; OPERATING SYSTEM : PC-DOS/MS-DOS
; SOFTWARE : Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER : US/08/485,778
; FILING DATE : 07-JE-1995
; CLASSIFICATION : 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER : US 08/387,524
; FILING DATE : 13-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER : US 08/330,123
; FILING DATE : 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER : US 08/272,102
; FILING DATE : 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME : Granahan, Patricia
; REGISTRATION NUMBER : 32,227
; REFERENCE/DOCKET NUMBER : CSLH94-05A4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE : 617-861-6240
; TELEFAX : 617-861-9540
; INFORMATION FOR SEQ ID NO: 1 :
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2425 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-485-778-1

Query Match          96.3% ; Score 834.6 ; DB 2 ; Length 2425 ;
Best Local Similarity 99.0% ; Pred No. 3,9e+259 ;
Matches    862 ; Conservative   0 ; Mismatches    4 ; Indels    5 ; Gaps    2

QY      1 AGCTACTCAGAGGCGTGTGACACAGCAAAATCCGTTGAACCCGGAGGACAGAGTGCGAGTG 60
       |||||||
Db      662 AGCTACTCAGAGGCGTGTGACACAGCAAAATCCGTTGAACCCGGGA-GCAGAGGTTGCAGTG 720

QY      61 AGCCGAGATCACGCCACATGACTCCATCCAGCGCTGGGCGAAAGACAGACATCCGTCCTCA 120
       |||||||
Db      721 AGCCGAGATCACGCCACATGACTCCATCCAGCGCTGGGCGAAAGACAGACATCCGTCCTCA 780

QY      121 AAAAAAAAAAACCTTAACATTATATGATGATATACATCCCTCTTTTACTCATCAAGACA 180
       |||||||
Db      781 AAAAAAAAAAACCTTAACATTATATGATGATATACATCCCTCTTTTACTCATCAAGACA 840

QY      181 CAGCACTACTTAAAGCAAAGTCATGATGAAACGCCCTTCTTCCATATAAAGGAGG 240
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Db      841  CAGCACACTACTTTAAAGCAAAAGTCATTAATGATTGAACACCCTTTCTTCTCTTAATAAAGGAG  900
Oy      241  ATTCAGTCTTTAAGATTAAATATGATAGTAGTACACTTGATTAAAGCCATCCTCTGTCTCA  300
Db      901  ATTCACTGCTCTTAAGATTAAATATGATAGTAGTACACTTGATTAAAGCCATCCTCTGTCTCA  960
Oy      301  AGGAAAGCTGTGGAGAAGGCAATTCTTAAGGAAAAAGGGGCAAGGTTGGAACTGTGGACGCATC  360
Db      961  AGGAGAGGCTGTGGAAAGGCAATTCTTAAGGAAAGAGGGGGGAGGGGTAGAACTCGGACGCATC  1020
Oy      361  CCACGTAGCCGAGCAGAGATTCTGTCTGTAGTCAAGTCTCTCTGGGAAATCTAATTTTCAACA  420
Db      1021  CCACTAGAGCCGAGCAGAGATTCTGTCTGTAGTCAAGTCTCTCTGGGAAATCTAATTTTCAACA  1080
Oy      421  AGTCTCTCCAAAAATGTGATGATCAAAACATGAGAAATTAAGTGTCTGTCTGTCTTAAGGCCCTA  480
Db      1081  AGTCTCTCCAAAAATGTGATGATCAAAACATGAGAAATTAAGTGTCTGTCTGTCTTAAGGCCCTA  1140
Oy      481  AAATCTTCTGTGATTTCCATTTTTTAAGGTAGTTCGAGGTGAACCCGCTGTGCTGTGCAGA  540
Db      1141  AAATCTTCTGTGATTTCCATTTTTTAAGGTAGTTCGAGGTGAACCCGCTGTGCTGTGCAGA  1200
Oy      541  GGATAGAAAAAAGGCCCTCTGATACCCCAAGTGAATTTACCTTTAAAGAAAGTCGCGAG  600
Db      1201  GGATAGAAAAAAGGCCCTCTGATACCTCAAGTAGTTTACCTTTAAAGAAAGTCGCGAG  1260
Oy      601  TAAAGACGCAAAAGCCTTTCCCGGAGCGTGGGGAAGGGCAACGCTCTTCCTCATGCGCCGAA  660
Db      1261  TAAAGACGCAAAAGCCTTTCCCGGAGCGTGGGGAAGGGCAACGCTCTTCCTCATGCGCCGAA  1320
Oy      661  ATGGAATCTTAATTTCCCGCTTCCCGCCCAACACGCGCCGCGGAGAGATGACTCTACAGAG  720
Db      1321  ATGGAATCTTAATTTCCCGCTTCCCGCCCAACACGCGCCGCGGAGAGATGACTCTACAGAG  1380
Oy      721  AGCCGCGAGAGTCAAGCTTTGGCCCAATCCGAGCGGTGGCGGCGCGCTTATTAAGCCGA  780
Db      1381  AGCCGCGAGAGTCAAGCTTTGGCCCAATCCGAGCGGTGGCGGCGCGCTTATTAAGCCGA  1440
Oy      781  CTCGCCCGGAGCGCACCGGAGGTTC---GGAAGGATGGGCTTGGGAGGGGATGCTGGCCAT  836
Db      1441  CTCGCCCGGAGCGCACCGGAGGTTCGCGAGGAGGAGGGGTGGGCTTGGGAGGGGATGCTGGCCAT  1500
Oy      837  TTTTGTCTAACCTCTAAGTCAAGAGAGGCGCTA  867
Db      1501  TTTTGTCTAACCTCTAAGTCAAGAGAGGCGCTA  1531

RESULT 10
US-08-520-550A-1
; Sequence 1, Application US/08520550A
; Patent No. 6013468
; GENERAL INFORMATION:
; APPLICANT: Andrews, William H.
; APPLICANT: Avillion, Ariel A.
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Greider, Carol
; APPLICANT: Marhuenda, Maria A. B.
; APPLICANT: Villeponteau, Bryant
; TITLE OF INVENTION: RNA Component of Telomerase
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

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: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/520,550A
: FILING DATE: 29-AUG-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/387,524
: FILING DATE: 13-FEB-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/330,123
: FILING DATE: 27-OCT-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/272,102
: FILING DATE: 07-JUL-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Granahan, Patricia
: REGISTRATION NUMBER: 32,227
: REFERENCE/DOCKET NUMBER: CSHL94-05A3B
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 617-861-9540
: TELEFAX: 617-861-6240
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2425 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
US-08-520-550A-1

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Query Match          96.3%; Score 834.6; DB 3; Length 2425;
Best Local Similarity 99.0%; Pred. No. 3.9e-259;
Matches 862; Conservative 0; Mismatches 4; Indels 5; Gaps 2;

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QY 1 AGCTACTCAGAGGCGTACAGAGAGAAATCGCTTGAACCCCGGAGGAGGTTGCGAGT 60
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DB 662 AGCTACTCAGAGGCGTACAGAGAGAAATCGCTTGAACCCCGGAGGAGGTTGCGAGT 720
    |||||||
QY 61 AGCCGAGATCAGCGCACTTAACCTCAGCCGCTGGGCGAAGAGCAAGCTCCGCTCA 120
    |||||||
DB 721 AGCCGAGATCAGCGCACTTAACCTCAGCCGCTGGGCGAAGAGCAAGCTCCGCTCA 780
    |||||||
QY 121 AAAAAAAAAATCGTTACAAATTTATGTTGATTAAGTCTCCCTCTTTTACATCAGACA 180
    |||||||
DB 781 AAAAAAAAAATCGTTACAAATTTATGTTGATTAAGTCTCCCTCTTTTACATCAGACA 840
    |||||||
QY 181 CAGCAGCTTAAAGCAATGATTAAGCAAGCGCTTTCTTCTAATAAAGGAG 240
    |||||||
DB 841 CAGCAGCTTAAAGCAATGATTAAGCAAGCGCTTTCTTCTAATAAAGGAG 900
    |||||||
QY 241 ATTCACTCTTAAGATTAATATGATTAAGTACCTTGAATTAAGCAATCCCTGCTCA 300
    |||||||
DB 901 ATTCACTCTTAAGATTAATATGATTAAGTACCTTGAATTAAGCAATCCCTGCTCA 960
    |||||||
QY 301 AGGAGAGCTGAGAGAGCAATCTTAAGGAAAAAGGGGAGGTTGAATCGAGCGCATC 360
    |||||||
DB 961 AGGAGAGCTGAGAGAGCAATCTTAAGGAAAAAGGGGAGGTTGAATCGAGCGCATC 1020
    |||||||
QY 361 CCACTGAGCCGAGAGCAATCTTCTGCTAGTCACTGCTGGGAGTCAATTTTCACAA 420
    |||||||
DB 1021 CCACTGAGCCGAGAGCAATCTTCTGCTAGTCACTGCTGGGAGTCAATTTTCACAA 1080
    |||||||
QY 421 AGTTCTCAAAAAATGATGATCAAAACTAGGAATTAAGTCTGCTGCTAGGCCCTTA 480
    |||||||
DB 1081 AGTTCTCAAAAAATGATGATCAAAACTAGGAATTAAGTCTGCTGCTAGGCCCTTA 1140
    |||||||
QY 481 AAATCTCTCTGTAATTCATTTTAAAGTAGTGAAGTGAACCGCTGCTGCTGAGA 540
    |||||||
DB 1141 AAATCTCTCTGTAATTCATTTTAAAGTAGTGAAGTGAACCGCTGCTGCTGAGA 1200
    |||||||
QY 541 GGATAGAAAAAGGCGCTGATACCTCAAGTTAGTTTCACTTTAAAGAGGTGCGAAG 600
    |||||||
DB 1201 GGATAGAAAAAGGCGCTGATACCTCAAGTTAGTTTCACTTTAAAGAGGTGCGAAG 1260
    |||||||

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QY 601 TAAAGACGAAAGCCCTTCCCGGACGTGGCGAAGGCGCAACGCTTCTCATGCGCGAA 660
    |||||||
DB 1261 TAAAGACGAAAGCCCTTCCCGGACGTGGCGAAGGCGCAACGCTTCTCATGCGCGAA 1320
    |||||||
QY 661 ATGGAACCTTTAATTTCCCGTTCGCCCAACACGCGCGCGAGAGAGTCACTCAACGAG 720
    |||||||
DB 1321 ATGGAACCTTTAATTTCCCGTTCGCCCAACACGCGCGCGAGAGAGTCACTCAACGAG 1380
    |||||||
QY 721 AGCCGAGAGTACAGCTTGGCCAAATCGGTGGGCGGCGCGCTCCCTTATTAAGCGGA 780
    |||||||
DB 1381 AGCCGAGAGTACAGCTTGGCCAAATCGGTGGGCGGCGCGCTCCCTTATTAAGCGGA 1440
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QY 781 CTCGCCGCGAGCGCACCGGCGTTGC---GGAGGTTGGCTGGAGAGGTTGGCCAT 836
    |||||||
DB 1441 CTCGCCGCGAGCGCACCGGCGTTGGCGAGGAGGTTGGCTGGAGAGGTTGGCCAT 1500
    |||||||
QY 837 TTTTGTCTAACCTTAACGAGAGGCGCTA 867
    |||||||
DB 1501 TTTTGTCTAACCTTAACGAGAGGCGCTA 1531
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RESULT 11
US-08-714-482-2
: Sequence 2, Application US/08714482
: Patent No. 5972605
: GENERAL INFORMATION:
: APPLICANT: Villeponteau, Bryant
: TITLE OF INVENTION: Assays for Regulators of Mammalian
: TITLE OF INVENTION: Telomerase Expression
: NUMBER OF SEQUENCES: 2
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend and Crew LLP
: STREET: Two Embarcadero Center, Eighth Floor
: CITY: San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94111-3834
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/714,482
: FILING DATE: 16-SEP-1996
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/521,634
: FILING DATE: 31-AUG-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/482,115
: FILING DATE: 07-JUN-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/472,802
: FILING DATE: 07-JUN-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/330,123
: FILING DATE: 27-OCT-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/272,102
: FILING DATE: 07-JUL-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Storella, John R.
: REGISTRATION NUMBER: 32,944
: REFERENCE/DOCKET NUMBER: 015389-00860US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 576-0200
: TELEFAX: (415) 576-0300
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 981 base pairs
: TYPE: nucleic acid

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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY:
LOCATION: 1..981
OTHER INFORMATION: /note="PstI fragment containing htr"
OTHER INFORMATION: sequence"
US-08-714-482-2

Query Match          38.5%; Score 334; DB 2; Length 981;
Best Local Similarity 100.0%; Pred. No. 8e-98;
Matches 334; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 534 CTCGAGAGATAGAAAAAGCCCTCTGATACCTCAAGTTAGTTTACCTTTAAAGAG 593
DB 1 CTCGAGAGATAGAAAAAGCCCTCTGATACCTCAAGTTAGTTTACCTTTAAAGAG 60
QY 594 TCGGAATGAAGACGCAAGCCTTTCCCGAGCGTGGGAAGGGCAAGTCTTCATG 653
DB 61 TCGGAATGAAGACGCAAGCCTTTCCCGAGCGTGGGAAGGGCAAGTCTTCATG 120
QY 654 GCCGGAATGAAGACTTAAATTTCCGTTCCCGCAACACGCGCCGAGAGAGTGAATC 713
DB 121 GCCGGAATGAAGACTTAAATTTCCGTTCCCGCAACACGCGCCGAGAGAGTGAATC 180
QY 714 TCAGAGAGCGCGAGAGTGAAGTGTGCGCAATCCGTGCGTGGCGCGCTCCCTTAT 773
DB 181 TCAGAGAGCGCGAGAGTGAAGTGTGCGCAATCCGTGCGTGGCGCGCTCCCTTAT 240
QY 774 AACCGACTGCGCGGAGCGGCAACCGGTTGCGAGAGGTGGGCTGGAGGGGTGGTGGC 833
DB 241 AACCGACTGCGCGGAGCGGCAACCGGTTGCGAGAGGTGGGCTGGAGGGGTGGTGGC 300
QY 834 CATTTTGTCTAACCTTAACCTAAGAGGCGCTA 867
DB 301 CATTTTGTCTAACCTTAACCTAAGAGGCGCTA 334

RESULT 12
US-08-710-249-5
Sequence 5, Application US/08710249
Patent No. 5858777
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Methods and Reagents for Regulating
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/710,249
FILING DATE: 13-SEP-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/583,808
FILING DATE: 05-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/003,492
FILING DATE: 08-SEP-1995
```

```
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-001220US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 981 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: misc-RNA
LOCATION: 267..715
OTHER INFORMATION:
OTHER INFORMATION: /product="htr"
OTHER INFORMATION: /note="htr transcript serves as
template in the telomerase
OTHER INFORMATION: ribonucleoprotein"
US-08-710-249-5

Query Match          38.4%; Score 333; DB 2; Length 981;
Best Local Similarity 99.7%; Pred. No. 1.7e-97;
Matches 333; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 534 CTCGAGAGATAGAAAAAGCCCTCTGATACCTCAAGTTAGTTTACCTTTAAAGAG 593
DB 1 CTCGAGAGATAGAAAAAGCCCTCTGATACCTCAAGTTAGTTTACCTTTAAAGAG 60
QY 594 TCGGAATGAAGACGCAAGCCTTTCCCGAGCGTGGGAAGGGCAAGTCTTCATG 653
DB 61 TCGGAATGAAGACGCAAGCCTTTCCCGAGCGTGGGAAGGGCAAGTCTTCATG 120
QY 654 GCCGGAATGAAGACTTAAATTTCCGTTCCCGCAACACGCGCCGAGAGAGTGAATC 713
DB 121 GCCGGAATGAAGACTTAAATTTCCGTTCCCGCAACACGCGCCGAGAGAGTGAATC 180
QY 714 TCAGAGAGCGCGAGAGTGAAGTGTGCGCAATCCGTGCGTGGCGCGCTCCCTTAT 773
DB 181 TCAGAGAGCGCGAGAGTGAAGTGTGCGCAATCCGTGCGTGGCGCGCTCCCTTAT 240
QY 774 AACCGACTGCGCGGAGCGGCAACCGGTTGCGAGAGGTGGGCTGGAGGGGTGGTGGC 833
DB 241 AACCGACTGCGCGGAGCGGCAACCGGTTGCGAGAGGTGGGCTGGAGGGGTGGTGGC 300
QY 834 CATTTTGTCTAACCTTAACCTAAGAGGCGCTA 867
DB 301 CATTTTGTCTAACCTTAACCTAAGAGGCGCTA 334

RESULT 13
US-09-220-157A-5
Sequence 5, Application US/09220157A
Patent No. 6300110
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Methods and Reagents for Regulating
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/220,157A
; FILING DATE:
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/08/710,249
; FILING DATE: 13-SEP-1996
; APPLICATION NUMBER: US 08/583,808
; FILING DATE: 05-JAN-1996
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 60/003,492
; FILING DATE: 08-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-00122005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 981 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc_RNA
; LOCATION: 267..715
; OTHER INFORMATION: /note="hmr transcript serves as
; OTHER INFORMATION: template in the telomerase
; OTHER INFORMATION: ribonucleoprotein"
US-09-220-157A-5

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Query Match      38.4%; Score 333; DB 4; Length 981;
Best Local Similarity 99.7%; Pred. No. 1.7e-97;
Matches 333; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 534 CTGCAGAGATAGAAAAAGCCCTGTGATACCTCAAGTTAGTTTCACTTTAAAGAGG 593
DB 1 CTGCAGAGATAGAAAAAGCCCTGTGATACCTCAAGTTAGTTTCACTTTAAAGAGG 60
QY 594 TCGGAAGTAAAGACGCAAAACCTTTCCCGACGTGCGGAAGGCAACGTCCTTCATG 653
DB 61 TCGGAAGTAAAGACGCAAAACCTTTCCCGACGTGCGGAAGGCAACGTCCTTCATG 120
QY 654 GCGGGAATGGAACCTTTAATTTCCCGTCCCGCAACGCGCGCGGAGAGTGAATC 713
DB 121 GCGGGAATGGAACCTTTAATTTCCCGTCCCGCAACGCGCGCGGAGAGTGAATC 180
QY 714 TCACGAGAGCGCGGAGAGTGAATTTCCCGTCCCGCAACGCGCGCGGAGAGTGAATC 773
DB 181 TCACGAGAGCGCGGAGAGTGAATTTCCCGTCCCGCAACGCGCGCGGAGAGTGAATC 240
QY 774 AAGCGACTGCGCGGAGAGTGAATTTCCCGTCCCGCAACGCGCGCGGAGAGTGAATC 833
DB 241 AAGCGACTGCGCGGAGAGTGAATTTCCCGTCCCGCAACGCGCGCGGAGAGTGAATC 300
QY 834 CATTTTGTCTAACCTTAAGTGAAGGCGGTA 867
DB 301 CATTTTGTCTAACCTTAAGTGAAGGCGGTA 334

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RESULT 14
US-08-770-565-1
; Sequence 1, Application US/08770565
; Patent No. 5846723
; GENERAL INFORMATION:
; APPLICANT: Kim, Nam Woo

```

```

; APPLICANT: Wu, Fred
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ronald
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Methods for Detecting the RNA Component of
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,565
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-00230005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0300
; TELEFAX: 415-576-0200
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 981 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-770-565-1

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Query Match      38.3%; Score 332.4; DB 2; Length 981;
Best Local Similarity 99.7%; Pred. No. 2.6e-97;
Matches 333; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 534 CTGCAGAGATAGAAAAAGCCCTGTGATACCTCAAGTTAGTTTCACTTTAAAGAGG 593
DB 1 CTGCAGAGATAGAAAAAGCCCTGTGATACCTCAAGTTAGTTTCACTTTAAAGAGG 60
QY 594 TCGGAAGTAAAGACGCAAAACCTTTCCCGACGTGCGGAAGGCAACGTCCTTCATG 653
DB 61 TCGGAAGTAAAGACGCAAAACCTTTCCCGACGTGCGGAAGGCAACGTCCTTCATG 120
QY 654 GCGGGAATGGAACCTTTAATTTCCCGTCCCGCAACGCGCGCGGAGAGTGAATC 713
DB 121 GCGGGAATGGAACCTTTAATTTCCCGTCCCGCAACGCGCGCGGAGAGTGAATC 180
QY 714 TCACGAGAGCGCGGAGAGTGAATTTCCCGTCCCGCAACGCGCGCGGAGAGTGAATC 773
DB 181 TCACGAGAGCGCGGAGAGTGAATTTCCCGTCCCGCAACGCGCGCGGAGAGTGAATC 240
QY 774 AAGCGACTGCGCGGAGAGTGAATTTCCCGTCCCGCAACGCGCGCGGAGAGTGAATC 833
DB 241 AAGCGACTGCGCGGAGAGTGAATTTCCCGTCCCGCAACGCGCGCGGAGAGTGAATC 300
QY 834 CATTTTGTCTAACCTTAAGTGAAGGCGGTA 867
DB 301 CATTTTGTCTAACCTTAAGTGAAGGCGGTA 334

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RESULT 15
US-08-833-377-1
; Sequence 1, Application US/08833377
; Patent No. 5968506
; GENERAL INFORMATION:

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APPLICANT: Weinrich, Scott L.
APPLICANT: Atkinson III, Edward M.
APPLICANT: Lichtsteiner, Serge P.
APPLICANT: Vassero, Alain P.
APPLICANT: Pruzan, Ronald A.
APPLICANT: Kealey, James T.
TITLE OF INVENTION: Purified Telomerase
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,377
FILING DATE: 04-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/510,736
FILING DATE: 04-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-001110US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 981 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: -
LOCATION: 1..981
OTHER INFORMATION: /note="PsiI fragment of the 2.4 kb
OTHER INFORMATION: SauIII-HindIII fragment of clone 28-1"
US-08-833-377-1

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Query Match      38.3%; Score 332.4; DB 2; Length 981;
Best Local Similarity 99.7%; Pred. No. 2,6e-97;
Matches 333; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 534 CTGCAGAGGATAGAAAAAGCCCTCTGATACCTCAAGTTAGTTTCACTTTAAAGAAGG 593
DB 1 CTGCAGAGGATAGAAAAAGCCCTCTGATACCTCAAGTTAGTTTCACTTTAAAGAAGG 60
QY 594 TCGGAGTAAGACGCAACGCTTCCCGAGCGTCCGAGGAGGCAAGTCCTTCATG 653
DB 61 TCGGAGTAAGACGCAACGCTTCCCGAGCGTCCGAGGAGGCAAGTCCTTCATG 120
QY 654 GCCGGAATGAACTTAAATTCCTCCGTTCCCGCAACACAGCCGCCGAGAGAGTACTC 713
DB 121 GCCGGAATGAACTTAAATTCCTCCGTTCCCGCAACACAGCCGCCGAGAGAGTACTC 180
QY 714 TCACGAGAGCGCGAGAGTACGCTTGCCCAATCCGTGCGGTCGCGCGCTCCCTTTAT 773
DB 181 TCACGAGAGCGCGAGAGTACGCTTGCCCAATCCGTGCGGTCGCGCGCTCCCTTTAT 240
QY 774 AAGCCGACTCGCCGCGAGGCAACCGGTTGCGGAGGAGGAGGAGGAGGAGGAGGAGG 833
DB 241 AAGCCGACTCGCCGCGAGGCAACCGGTTGCGGAGGAGGAGGAGGAGGAGGAGGAGG 300
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DB 301 CATTTTGTCTAACCTAAGAGGAGGCTA 334

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Search completed: January 25, 2003, 13:43:36
Job time : 95 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 25, 2003, 13:43:40 ; Search time 3208 Seconds

(without alignments)
7865.378 Million cell updates/sec

Title: US-09-601-267-36

Perfect score: 867
Sequence: 1 agctactcagagagctgaga.....ccctactcagagagcgcta 867Scoring table: IDENTITY-NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	867	100.0	867	6	AX019582
2	867	100.0	1765	6	AX019582
3	867	100.0	1765	6	AF047386
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5	848.6	97.9	2420	6	131750
6	848.6	97.9	2426	6	AR016035
7	848.6	97.9	2426	6	AR059196
8	848.6	97.9	2426	6	AR075507
9	848.6	97.9	2426	6	AR081664
10	848.6	97.9	2426	6	AR161905
11	334	38.5	981	6	AR081665
12	333	38.4	981	6	AR028774
13	333	38.4	981	6	AX022166
14	332.4	38.3	981	6	AB4591
15	332.4	38.3	981	6	AR063825
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18	166	19.1	548	9	AF221907
19	163	18.8	545	9	HS086046
20	120	13.8	120	6	AX019627
21	117.2	13.5	157466	9	AC004888
22	115.6	13.3	70778	2	AC113136
23	115.6	13.3	165105	2	AC024240
24	114.2	13.2	197099	9	AL136979
25	114	13.1	115812	9	AC004796
26	113.6	13.1	176550	9	AL356356
27	112.6	13.0	39170	9	AC067969
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29	110.8	12.8	68275	9	AC073335
30	110.8	12.8	128501	9	AC012614
31	110.8	12.8	187495	9	AC026887
32	110.6	12.8	185574	9	AC073341
33	110.2	12.7	107037	9	HS1678E16
34	110	12.7	132912	9	AL358075
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38	109.4	12.6	149505	9	AC093767
39	109.4	12.6	193689	2	AC066603
40	109.4	12.6	211452	2	AP002010
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42	109.2	12.6	120917	9	HS1583P15
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ALIGNMENTS

RESULT 1
LOCUS AX019582 867 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 36 from Patent WO938964.
ACCESSION AX019582
VERSION AX019582.1 GI:10043496
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 867)
AUTHORS Kelth,W.N.
TITLE Promoter regions of the mouse and human telomerase rna component genes

JOURNAL Patent: WO 9938964-A 36 05-AUG-1999;
KEITH WILLIAM NICOL (GB); CANCER RES CAMPAIGN TECH (GB)
FEATURES Location/Qualifiers
source 1..867
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 237 a 209 c 221 g 200 t
ORIGIN

Query Match 100.0%; Score 867; DB 6; Length 867;
Best Local Similarity 100.0%; Pred. No. 5.5e-240;
Matches 867; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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181 CAGCACTACTTTAAAGCAAGTCAATGATTTGAAGAGCGCTTCTTCTTCTTCTTCTTCTTCT 240
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781 CTCGGCCCGGAGCGGAGTGGGAGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGG 840
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841 TGTCTAACCCTTACTGAGAAGGCGCTA 867
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RESULT 2
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LOCUS Sequence 1 from Patent WO9938964.
DEFINITION AX019547
ACCESSION AX019547.1 GI:10043461
VERSION
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1765)
AUTHORS Keith,W.N.
TITLE Promoter regions of the mouse and human telomerase rna component
JOURNAL Patent: WO 9938964-A 1 05-AUG-1999;
KEITH WILLIAM NICOL (GB); CANCER RES CAMPAIGN TECH (GB)
FEATURES Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 404 a 458 c 480 g 423 t
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Query Match 100.0%; Score 867; DB 6; Length 1765;
Best Local Similarity 100.0%; Pred. No. 6.2e-240;
Matches 867; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AGCTACTCAGAGGCGTGAGACAGAGAAATCGCTTGAACCGGGAGGAGAGGTTGAGAG 60
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QY 661 ATGGAATTATTTCCCTTCCCTCCCAACACACCCCGGAGAGATGACTCTCACGAG 720
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QY 721 AGCCGGAGAGTACAGTTGGCCCAATCCGTCGCGGCGCGCTCCCTTATTAAGCCGA 780
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Db 841 TGTCTAACCTTAAGTGAAGGCGCTA 867

RESULT 3
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LOCUS Homo sapiens telomerase RNA (TR) gene, promoter and complete
DEFINITION sequence.
ACCESSION AF047386
VERSION AF047386.1 GI:300555
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE 1 (bases 1 to 1765)
AUTHORS Zhao,J.Q., Hoare,S.F., McFarlane,R., Muir,S., Parkinson,E.K.,
Black,D.M. and Keith,W.N.
TITLE Cloning and characterization of human and mouse telomerase RNA gene
promoter sequences
JOURNAL Oncogene 16 (10), 1345-1350 (1998)
MEDLINE 98206512
PUBMED 9546436
REFERENCE 2 (bases 1 to 1765)
AUTHORS Zhao,J.Q., Hoare,S.F., McFarlane,R., Muir,S., Parkinson,E.K.,
Black,D.M. and Keith,W.N.
TITLE Direct Submission
JOURNAL Submitted (09-FEB-1998) Medical Oncology, Beatson Institute,
Switchback Rd, Glasgow G61 1BD, UK
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Best Local Similarity 100.0%; Pred. No. 6.2e-240;
Matches 867; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGTACTCAGGAGGTGAGACAGAGATCGTTGAACCGGAGGACAGAGTTGCAGTG 60
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Db 121 AAAAAAAAAATCGTTCATTTTATGGTGATTACTCCCTCTTTTAACTCATCAAGACA 180
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Db 181 CACACTACTTTTAAAGCAAGTCAATGATTGAAGCCCTTTTCTTCTATAAAGAGAG 240
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Db 241 ATTCACTCCTTAAGATTATATGATGATTAAGTGAAGTGAAGTGAAGTGAAGTGAAG 300
QY 301 AGGAGAGGTGGAGAGGATCTTAAGGAAAAAGGGGAGGGGTGAAGTGAAGTGAAGTGAAG 360
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Db 301 AGGAGAGGTGGAGAGGATCTTAAGGAAAAAGGGGAGGGGTGAAGTGAAGTGAAGTGAAG 360
QY 361 CCACGTAGCGGAGACAAAGATTCTGTAGTACGTCTGCTCGTGAATCAATTTTACAA 420
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Db 361 CCACGTAGCGGAGACAAAGATTCTGTAGTACGTCTGCTCGTGAATCAATTTTACAA 420
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RESULT 4
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LOCUS Homo sapiens chromosome 3 clone RP11-816u6, WORKING DRAFT SEQUENCE,
DEFINITION 2 unordered pieces.
ACCESSION AC078802
VERSION AC078802.11 GI:21397225
KEYWORDS HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE human.
ORGANISM Homo sapiens.
REFERENCE 1 (bases 1 to 145829)
AUTHORS Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alsbjrooks,S.L., AmaralLunge,H.C., Are,J.R., Ayele,M., Banks,T.,
Barbarta,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,
Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
Carroll,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
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Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
Earhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
Gabali, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K.,
Harris, C., Harris, K., Hart, M., Haylak, P., Hawes, A., Hernandez, J.,
Hernandez, O., Hodgson, A., Hognes, M., Holloway, C., Hollins, B.,
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Karlsso, E., Kelly, S., Khan, U., King, J., Kovach, J., Kovar, C.,
Krivovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.,
Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louised, H.,
Lozdo, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J.,
Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, F.,
Massey, E., McElroy, E., McLeod, M.P., Meador, M., Mel, G., Metzger, M.,
Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S.,
Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N.,
Nguyen, N., Nickerson, E., Nwokenkwo, S., Ogih, M., Okwuonu, G.,
Oragune, N., Oviedo, R., Pace, A., Payton, B., Peery, D., Perez, L.,
Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y.,
Rivas, M., Rojas, A., Rojiboken, I., Rolfe, M., Ruiz, S., Savery, G.,
Scheer, S., Scott, G., Shen, H., Shooshkat, N., Sisson, I.,
Sodergren, E., Sonalike, T., Sparks, A., Stanley, H., Stone, H.,
Sutton, A., Sytek, A., Taber, P., Tamerisa, A., Tamerisa, K., Tang, H.,
Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S.,
Usmani, K., Vasquez, L., Vera, V., Villalón, D., Vinson, R., Wang, O.,
Wang, S., Ward-Moore, S., Warren, R., Washington, C., Wallington, S.,
Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K.,
Wu, C., Wu, F., Wu, F., Zhou, J., Zorrilla, S., Nelson, D.,
Welnstock, G. and Gibbs, R.

Direct Submission
Unpublished
2 (bases 1 to 145829)
Morley, K.C.

Direct Submission
Submitted (04-AUG-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 145829)
Morley, K.C.

Direct Submission
Submitted (19-JUN-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jun 13, 2002 this sequence version replaced gi:20514648.

----- Genome Center

Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Drafting Center Code: BCM
Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: HRTU
Center clone name: RP11-816J6

----- Summary Statistics

Sequencing vector: M13
Chemistry: Dye-terminator Big Dye 65% of reads
Assembly program: Phrap, version 0.990329
Consensus quality: 145499 bases at least Q40
Consensus quality: 145597 bases at least Q30
Consensus quality: 145599 bases at least Q20
Estimated insert size: 148612: sum-of-contigs estimation
Quality coverage: 6x in Q20 bases: sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank/draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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8301 8400: gap of unknown length
8401 145829: contig of 137429 bp in length.
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/db_xref="taxon:9606"
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/clone="RP11-816J6"

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ORIGIN

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Best Local Similarity 99.5%; Pred. No. 9,4e-238;
Matches 863; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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241 ATTCACTCTTTAAAGTAAATGTAAGTAAATGTAAGTAAATGTAAGTAAATGTAAGTAA 300
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Db 143753 ATTCACTCTTTAAAGTAAATGTAAGTAAATGTAAGTAAATGTAAGTAAATGTAAGTAA 143694

301 AGGAGAAAGTGGAGAGGAGGATTTAGGAGAAAGGAGGAGGAGGAGGAGGAGGAGGAG 360
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Db 143693 AGGAGAAAGTGGAGAGGAGGATTTAGGAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 143634

361 CCACAGAGCGAGACAAAGATTTGCTGTAGTCAAGTCTCTCGGGAATGTTTTCACAA 420
|||||
Db 143633 CCACAGAGCGAGACAAAGATTTGCTGTAGTCAAGTCTCTCGGGAATGTTTTCACAA 143574

421 AGTTCTCCAAAAATGTGATGATCAAAACTAGGAATTTAGTTCTGTCTTAAAGCCCTTA 480
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Db 143573 AGTTCTCCAAAAATGTGATGATCAAAACTAGGAATTTAGTTCTGTCTTAAAGCCCTTA 143514

481 AATCTCTCTGTGAATTTTCAATTTTAAAGTACGAGGTGAACCGGTGTGCTGTCAGAA 540
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Db 143513 AATCTCTCTGTGAATTTTCAATTTTAAAGTACGAGGTGAACCGGTGTGCTGTCAGAA 143454

541 GGTATAGAAAAAGGCGCTCTGATACCTCAAGTTAGTTTACCTTTAAAGAGGTGGAG 600
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601 TAAAGAGCAAAAGCCTTTCCGAGAGCTGGGAGGAGCAAGTCCTTCATGAGCCGGA 660
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Db 143393 TAAAGAGCAAAAGCCTTTCCGAGAGCTGGGAGGAGCAAGTCCTTCATGAGCCGGA 143334

661 ATGGAACCTTAATTTCCGCTTCCGCAACGACCGCGCGGAGAGAGTACGTCACGAG 720
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Db 143333 ATGGAACCTTAATTTCCGCTTCCGCAACGACCGCGCGGAGAGAGTACGTCACGAG 143274

721 AGCCGAGAGATCAGCTTGGCAATCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
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Db 143273 AGCCGAGAGATCAGCTTGGCAATCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 143214

781 CTCGCGGCGAGCGACCGCGGTTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
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Db 143213 CTCGCCGCGAGCGACACCGGGCTTCCGAGGGTGGCCCTGGAGGGTGCTGGCCATTTT 143154

QY 841 TGTCTAACCTTAAGTGAAGGCGCTA 867
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Db 143153 TGTCTAACCTTAAGTGAAGGCGCTA 143127

RESULT 5
LOCUS 131750 2420 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 3 from patent US 5583016.
ACCESSION 131750
VERSION 131750.1 GI:1822541
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 2420)
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE Mammalian telomerase
JOURNAL Patent: US 5583016-A 3 10-DEC-1996:
FEATURES Location/Qualifiers
source 1..2420
BASE COUNT 620 a 572 c 647 g 581 t
ORIGIN

Query Match 97.9%; Score 848.6; DB 6; Length 2420:
Best Local Similarity 99.4%; Pred. No. 1.4e-234;
Matches 862; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

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QY 61 AGCCGAGATCAGCCCACTAGACTCCATCCAGCTGGCGAAAGCAAGCACTCCGTCTCA 120
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Db 721 AGCCGAGATCAGCCCACTAGACTCCATCCAGCTGGCGAAAGCAAGCACTCCGTCTCA 780

QY 121 AAAAAAAAAATCGTTCAATTTATGGGATTACTCCCTTTTAACTCATCAAGACA 180
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Db 781 AAAAAAAAAATCGTTCAATTTATGGGATTACTCCCTTTTAACTCATCAAGACA 840

QY 181 CAGCACTACTTTAAAGCAATGATGATGAAGCGCTTTCTTCTCTAATAAAGGAG 240
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Db 841 CAGCACTACTTTAAAGCAATGATGATGAAGCGCTTTCTTCTCTAATAAAGGAG 900

QY 241 ATTCACTCTTTAAGATTAAATGATGATGATGATGATGATGATGATGATGATGATGAT 300
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Db 901 ATTCACTCTTTAAGATTAAATGATGATGATGATGATGATGATGATGATGATGATGAT 960

QY 301 AGGAGAACTGGAGAAAGGCTTTCTAAGGAAAAAGGGGAGGGTTGGAACTCGGAGCATC 360
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Db 961 AGGAGAACTGGAGAAAGGCTTTCTAAGGAAAAAGGGGAGGGTTAGGAACTCGGAGCATC 1020

QY 361 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAAGTGCCTGGCGAATCTAATTTTCACAA 420
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Db 1021 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAAGTGCCTGGCGAATCTAATTTTCACAA 1080

QY 421 AGTTTCTCAAAAAATGATGATCAAAACTAGAAATTAGTGTCTGTGTTTAAAGCCCTTA 480
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Db 1081 AGTTTCTCAAAAAATGATGATCAAAACTAGAAATTAGTGTCTGTGTTTAAAGCCCTTA 1140

QY 481 AAATCTCTCTGTAATTCATATTTTAAAGTAGTAGAGTAGAGTAGAGTAGAGTAGAGTAGAG 540
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Db 1141 AAATCTCTCTGTAATTCATATTTTAAAGTAGTAGAGTAGAGTAGAGTAGAGTAGAGTAGAG 1200

QY 541 GGATAGAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACTTTTAAAGAGAGTGGAGAG 600
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Db 1321 ATGAACATTAAATTTCCCGTTCCCGCAACACAGCCGCCGAGAGATGACTCTACAGAG 1380

QY 721 AGCCGAGAGTCAAGCTTGGCCAATCCGTGCGGTGGCGGCCGCTCCCTTATTAAGCCGA 780
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Db 1381 AGCCGAGAGTCAAGCTTGGCCAATCCGTGCGGTGGCGGCCGCTCCCTTATTAAGCCGA 1440

QY 781 CTCGCCCGGAGCGACACCGGTTGCGGAGGTTGGGCTGGGAGAGGTTGGTGGCCATTTT 840
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QY 841 TGTCTAACCTTAAGTGAAGGCGCTA 867
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Db 1501 TGTCTAACCTTAAGTGAAGGCGCTA 1527

RESULT 6
LOCUS AR016035 2426 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 3 from patent US 5776679.
ACCESSION AR016035
VERSION AR016035.1 GI:3972312
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 2426)
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE Assays for the DNA component of human telomerase
JOURNAL Patent: US 5776679-A 3 07-JUL-1998:
FEATURES Location/Qualifiers
source 1..2426
BASE COUNT 620 a 575 c 650 g 581 t
ORIGIN

Query Match 97.9%; Score 848.6; DB 6; Length 2426:
Best Local Similarity 99.4%; Pred. No. 1.4e-234;
Matches 862; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 AGCTACTCAGAGCGCTGAGACAGAGATCGCTTGAACCCGGAGCGAGAGTTGCAGTG 60
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Db 662 AGCTACTCAGAGCGCTGAGACAGAGATCGCTTGAACCCGGAG -GCAGAGTTGCAGTG 720

QY 61 AGCCGAGATCAGCCCACTAGACTCCATCCAGCTGGCGAAAGCAAGCACTCCGTCTCA 120
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Db 721 AGCCGAGATCAGCCCACTAGACTCCATCCAGCTGGCGAAAGCAAGCACTCCGTCTCA 780

QY 121 AAAAAAAAAATCGTTCAATTTATGGGATTACTCCCTTTTAACTCATCAAGACA 180
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Db 781 AAAAAAAAAATCGTTCAATTTATGGGATTACTCCCTTTTAACTCATCAAGACA 840

QY 181 CAGCACTACTTTAAAGCAATGATGATGAAGCGCTTTCTTCTCTAATAAAGGAG 240
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Db 841 CAGCACTACTTTAAAGCAATGATGATGAAGCGCTTTCTTCTCTAATAAAGGAG 900

QY 241 ATTCACTCTTTAAGATTAAATGATGATGATGATGATGATGATGATGATGATGATGAT 300
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Db 901 ATTCACTCTTTAAGATTAAATGATGATGATGATGATGATGATGATGATGATGATGAT 960

QY 301 AGGAGAACTGGAGAAAGGCTTTCTAAGGAAAAAGGGGAGGGTTGGAACTCGGAGCATC 360
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Db 961 AGGAGAACTGGAGAAAGGCTTTCTAAGGAAAAAGGGGAGGGTTAGGAACTCGGAGCATC 1020

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Db 1441 CTCGCCCCGACGCGACCGGGTTGCGGAGGGTGGGCTGGGAGGGGTGGTGGCCATTTT 1500
Qy 841 TGTCTAACCTTAACCTGAGAAAGGCGCTA 867
Db 1501 TGTCTAACCTTAACCTGAGAAAGGCGCTA 1527

RESULT 7
AR059196 2426 bp DNA linear PAT 29-SEP-1999
LOCUS AR059196
DEFINITION Sequence 3 from patent US 5837857.
ACCESSION AR059196
VERSION AR059196.1 GI:5984773
KEYWORDS
SOURCE .
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2426)
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE Mammalian telomerase
JOURNAL Patent: US 5837857-A 3 17-NOV-1998;
FEATURES
source 1..2426
/organism="unknown"
BASE COUNT 620 a 575 c 650 g 581 t
ORIGIN

Query Match 97.9%; Score 848.6; DB 6; Length 2426;
Best Local Similarity 99.4%; Pred. No. 1.4e-234;
Matches 862; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
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Db 901 ATTCACTCCTTAAGATTAAATGATAGTAGTATACACTGTATTAAAGCATCCTGCTCA 960
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Qy 361 CCACTAGGCGGAGACAAAGATTCTGCTGTAGTCAGTCTCCCTGGGAATCTATTTTCACA 420
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Db 1201 GGATAGAAAAAGGCGCTGTGATACCTCAAGTTAGTTTACCTTTAAAGAAAGTCCGAAG 1260
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Db 1261 TAAAGACGCAAAAGCCCTTCCCGGAGCTGCGGAAGGGCAACGCTCTTCTCATGCGCGGAA 1320
Qy 661 ATGGAACCTTAATTTCCGCTTCCCGCAACCGCGCCGAGAGTGAATGACTCTCAAGAG 720
Db 1321 ATGGAACCTTAATTTCCGCTTCCCGCAACCGCGCCGAGAGTGAATGACTCTCAAGAG 1380
Qy 721 AGCCGCGAGAGTCAGCTTGGCCAAATCCGTGCGGTCGGCGCGCTCCCTTTATAAGCCGA 780
Db 1381 AGCCGCGAGAGTCAGCTTGGCCAAATCCGTGCGGTCGGCGCGCTCCCTTTATAAGCCGA 1440
Qy 781 CTCGCCCCGACGCGACCGGGTTGCGGAGGGTGGGCTGGGAGGGGTGGTGGCCATTTT 840
Db 1441 CTCGCCCCGACGCGACCGGGTTGCGGAGGGTGGGCTGGGAGGGGTGGTGGCCATTTT 1500
Qy 841 TGTCTAACCTTAACCTGAGAAAGGCGCTA 867
Db 1501 TGTCTAACCTTAACCTGAGAAAGGCGCTA 1527

RESULT 8
AR075507 2426 bp DNA linear PAT 30-AUG-2000
LOCUS AR075507
DEFINITION Sequence 4 from patent US 5958680.
ACCESSION AR075507
VERSION AR075507.1 GI:1002257
KEYWORDS
SOURCE .
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2426)
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE Mammalian telomerase
JOURNAL Patent: US 5958680-A 4 28-SEP-1999;
FEATURES
source 1..2426
/organism="unknown"
BASE COUNT 620 a 575 c 650 g 581 t
ORIGIN

Query Match 97.9%; Score 848.6; DB 6; Length 2426;
Best Local Similarity 99.4%; Pred. No. 1.4e-234;
Matches 862; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
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 Db 781 AAAAAAAAAATGTTAAATTTATGGTATTAATCTCCCTCTTTTAACTCATCAAGACA 840
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 Db 841 CAGCACTACTTTAAAGCAAGTCAATGATTTGAAGCCCTTTCTTCTATATAAAGGAG 900
 QY 241 ATTCACTCTTAAAGTATTAATATGATGATTTACACTTGAATTAAGCCATCTCTCTCA 300
 Db 901 ATTCACTCTTAAAGTATTAATATGATGATTTACACTTGAATTAAGCCATCTCTCTCA 960
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 Db 961 AGAGAGAGCTGGAGAGGCAATTTCTAAGGAAAAAGGGGAGGTTGGAACTCGAGCATC 1020
 QY 361 CCACTGAGCCGAGACAAGATTTCTGTAGTCAAGTGTGCTGGGGAATCTATTTTCACAA 420
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 Db 1081 AGTTCTCCAAAAATGATGATCAAAACTAGAAATTAAGTGTCTGTCTTAAAGCCCTA 1140
 QY 481 AATCTTCTGTGAATTTCCATTTTAAAGTATGAGTGAAGTCAAGTGTCTGTCTGAGA 540
 Db 1141 AATCTTCTGTGAATTTCCATTTTAAAGTATGAGTGAAGTCAAGTGTCTGTCTGAGA 1200
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 Db 1201 GGATAGAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACTTTAAAGAGTCCGGAAG 1260
 QY 601 TAAAGAGCGCAAGCCTTTCCCGGAGCTGGCGAAGGGCAAGCTCTCTATAGCCGGA 660
 Db 1261 TAAAGAGCGCAAGCCTTTCCCGGAGCTGGCGAAGGGCAAGCTCTCTATAGCCGGA 1320
 QY 661 ATGGAATTTAATTTCCCGTTCGCCCAACAGCCGCGGAGAGAGTCACTCTCAAGAG 720
 Db 1321 ATGGAATTTAATTTCCCGTTCGCCCAACAGCCGCGGAGAGAGTCACTCTCAAGAG 1380
 QY 721 AGCCGAGAGTCAAGTGTGCGCAATCGTGCGGCGCGCTCCCTTTATTAAGCCGA 780
 Db 1381 AGCCGAGAGTCAAGTGTGCGCAATCGTGCGGCGCGCTCCCTTTATTAAGCCGA 1440
 QY 781 CTGCGCCGCGAGCGCACCGGGTTCGGAGAGGTGGAGGGTGTGGCCATTTT 840
 Db 1441 CTGCGCCGCGAGCGCACCGGGTTCGGAGAGGTGGAGGGTGTGGCCATTTT 1500
 QY 841 TGTCTAACCTTAAGTGAAGGGCGTA 867
 Db 1501 TGTCTAACCTTAAGTGAAGGGCGTA 1527
 RESULT 9
 ARO81664 LOCUS 2426 bp DNA linear PAT 31-AUG-2000
 DEFINITION Sequence 1 from patent US 5972605.
 ACCESSION ARO81664
 VERSION ARO81664.1 GI:10008390
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 2426)
 AUTHORS Villeponteu, B. and Harley, C.
 TITLE Assays for regulators of mammalian telomerase expression
 JOURNAL Patent: US 5972605-A 1 26-OCT-1999.
 FEATURES
 source location/Qualifiers
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 /organism="unknown"
 BASE COUNT 620 a 575 c 650 g 581 t

ORIGIN
 Query Match 97.9%; Score 848.6; DB 6; Length 2426;
 Best Local Similarity 99.4%; Pred. No. 1.4e-234;
 Matches 862; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
 QY 1 AGTACTCAGAGAGCTGAGACACAGAGAAATCGCTGAACCCGGGAGGACAGAGTTCCAGTG 60
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 QY 61 AGCCGAGATCAGCGCCACTGACATCCATCCAGCTGGGCGAAGAGCAACACTCCGTCTCA 120
 Db 721 AGCCGAGATCAGCGCCACTGACATCCATCCAGCTGGGCGAAGAGCAACACTCCGTCTCA 780
 QY 121 AAAAAAAAAATGTTAAATTTATGGTATTAATCTCCCTCTTTTAACTCATCAAGACA 180
 Db 781 AAAAAAAAAATGTTAAATTTATGGTATTAATCTCCCTCTTTTAACTCATCAAGACA 840
 QY 181 CAGCACTACTTTAAAGCAAGTCAATGATTTGAAGCCCTTTCTTCTATATAAAGGAG 240
 Db 841 CAGCACTACTTTAAAGCAAGTCAATGATTTGAAGCCCTTTCTTCTATATAAAGGAG 900
 QY 241 ATTCACTCTTAAAGTATTAATATGATGATTTACACTTGAATTAAGCCATCTCTCTCA 300
 Db 901 ATTCACTCTTAAAGTATTAATATGATGATTTACACTTGAATTAAGCCATCTCTCTCA 960
 QY 301 AGAGAGAGCTGGAGAGGCAATTTCTAAGGAAAAAGGGGAGGTTGGAACTCGAGCATC 360
 Db 961 AGAGAGAGCTGGAGAGGCAATTTCTAAGGAAAAAGGGGAGGTTGGAACTCGAGCATC 1020
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 QY 601 TAAAGAGCGCAAGCCTTTCCCGGAGCTGGCGAAGGGCAAGCTCTCTATAGCCGGA 660
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 RESULT 10
 ARI61905 LOCUS 2426 bp DNA linear PAT 17-OCT-2001
 DEFINITION Sequence 3 from patent US 6258535.
 ACCESSION ARI61905
 VERSION ARI61905.1 GI:16228915

KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 2426)
AUTHORS	Villeponteau, B., Feng, J., Funk, W. and Andrews, W.H.
TITLE	Mammalian telomerase
JOURNAL	Patent: US 6258535-A 3 10-JUL-2001;
FEATURES	Location/Qualifiers
source	1..2426
BASE COUNT	620 a 575 c 650 g 581 t
ORIGIN	/organism="unknown"
Query Match	97.9% ; Score 848.6; DB 6; Length 2426;
Best Local Similarity	99.4% ; Pred. No. 1.4e-234;
Matches 862; Conservative	0; Mismatches 4; Indels 1; Gaps 1.
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QY	121 AAAAAAAAAATCGTTACATTTATGGTGATTAATCCCTCTTTTACCTCAAGACA 180
DB	781 AAAAAAAAAATCGTTACATTTATGGTGATTAATCCCTCTTTTACCTCAAGACA 840
QY	181 CAGCACTACTTTAAAGCAAGTCAATGATGAACGCCCTTTCTTTCTTAATAAAGGAG 240
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QY	841	TGCTTAACCCCTACTAGAGAAGGGCGTGA	867
Db	1501	TGCTTAACCCCTAACTAGAGAAGGGCGCTA	1527
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ACCSSION	AR081665		PAT 31-AUG-2000
VERSION	AR081665.1	GI:10008391	
KEYWORDS			
SOURCE	unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 981)		
AUTHORS	Villepoiteau,B., Feng,J., Andrews,W.H. and Adams,R.R.		
TITLE	Assays for regulators of mammalian telomerase expression		
JOURNAL	Patent: US 5972605-A 2 26-OCT-1999;		
FEATURES	Location/Qualifiers		
source	1..981		
BASE COUNT	172 a 303 c 306 g 200 t		
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QY	534	CTGCAGAGATGTGAAAAAAGGCCCTCATATCCCAAGTTAGTTTCACCTTTAAAGAAG	593
Db	1	CTGCAGAGAGATGAAAAAAGGCCCTCATATCCTCAATTAGTTTCACCTTTAAAGAAG	60
QY	594	TCGGAAGTAAACAGCSCAAAGCCTTTCCCGAGCGTGCGGAAGGCAACCTCCTTCATYG	653
Db	61	TCGGAAGTAAAGAACSCCAAAGCCTTTCCCGAGCGTGCGGAAGGCAACGCTTCCTCATG	120
QY	654	GCCGGAATGGAACCTTTAATTTCCCGTTCCCCCACACGAGCCGCCGAGAGAGTAGCTC	713
Db	121	GCCGGAATGGAACCTTTAATTTCCCGTTCCCCCACACGAGCCGCCGAGAGAGTAGCTC	180
QY	714	TCACAGAGACCGCGAGAGCTAGCTTGCCCAATCCGTGGCGTTCGGCGCCGCTCCCTTTAT	773
Db	181	TCACAGAGACCGCGAGAGCTAGCTTGCCCAATCCGTGGCGTTCGGCGCCGCTCCCTTTAT	240
QY	774	AAGCCGACTCGCCCGCGAGCGCACCCGGSTTCGAGAGGTGGGCGGTGGGTGGC	833
Db	241	AAGCCGACTCGCCCGCGAGCGCACCCGGSTTCGAGAGGTGGGCGGTGGGTGGC	300
QY	834	CATTTTGTCTAACCCCTAACTAGAGAAGGGCGTGA	867
Db	301	CATTTTGTCTAACCCCTAACTAGAGAAGGGCGTGA	334
RESULT 12			
AR028774			
LOCUS	AR028774	981 bp	DNA
DEFINITION	Sequence 5 from patent US 5858777.		Linear
ACCSSION	AR028774		PAT 29-SEP-1999
VERSION	AR028774.1	GI:5940747	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 981)		
TITLE	Villepoiteau,B., Feng,J., Andrews,W.H. and Adams,R.R.		
JOURNAL	Methods and reagents for regulating telomere length and telomerase activity		
FEATURES	Patent: US 5858777-A 5 12-JAN-1999;		
source	Location/Qualifiers		
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	/organism="unknown"		

BASE COUNT 172 a 303 c 305 g 200 t 1 others
ORIGIN

Query Match 38.4%; Score 333; DB 6; Length 981;
Best Local Similarity 99.7%; Pred. No. 2.5e-85;
Matches 333: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 534 CTGCAGAGATGAAAAAGGCCCTCTGATACCTCAAGTTAGTTTACCTTTAAAGAGG 593
DB 1 CTGCAGAGATGAAAAAGGCCCTCTGATACCTCAAGTTAGTTTACCTTTAAAGAGG 60

QY 594 TCGGAAGTAAAGACGCAAGCCTTTCCCGAGCTGGGAAAGGCAACGTCCTTCATG 653
DB 61 TCGGAAGTAAAGACGCAAGCCTTTCCCGAGCTGGGAAAGGCAACGTCCTTCATG 120

QY 654 GCCGGAATGGAACCTTAATTTCCCGTTCCCGCAACGAGCCCGCGAGAGTACTC 713
DB 121 GCCGGAATGGAACCTTAATTTCCCGTTCCCGCAACGAGCCCGCGAGAGTACTC 180

QY 714 TCACGAGACCCGCGAGAGTCAGCTTGGCAATCCGTCGGCGCGCTCCCTTTAT 773
DB 181 TCACGAGACCCGCGAGAGTCAGCTTGGCAATCCGTCGGCGCGCTCCCTTTAT 240

QY 774 AAGCCGACTCGCCCGGCAACGCGAGCGGTTGGGAGGTTGGCTTGGAGGGGTGGTGC 833
DB 241 AAGCCGACTCGCCCGGCAACGCGAGCGGTTGGGAGGTTGGGAGGGGTGGTGC 300

QY 834 CATTTTGTCTTAACCTTAACCTTAACCTTAACCTTAACCTTAACCTTAACCTTA 867
DB 301 CATTTTGTCTTAACCTTAACCTTAACCTTAACCTTAACCTTAACCTTAACCTTA 334

RESULT 13
AX022166

LOCUS AX022166 981 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 5 from Patent EP0953042.
ACCESSION AX022166
VERSION AX022166.1 GI:10045843
KEYWORDS
SOURCE .
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 981)
AUTHORS Andrews,M.H., Villeponteau,B., Adams,R.R. and Feng,J.
TITLE Methods and reagents for regulating telomere length and telomerase activity
JOURNAL Patent: EP 0953042-A 5 03-NOV-1999;
GERON CORP (US)

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source Location/Qualifiers
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/organism="unidentified"
/db_xref="taxon:32644"
misc_RNA .
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/product="HTR"
/note="HTR TRANSCRIPT SERVES AS TEMPLATE IN THE TELOMERASE RIBONUCLEOPROTEIN"

BASE COUNT 172 a 303 c 305 g 200 t 1 others
ORIGIN

Query Match 38.4%; Score 333; DB 6; Length 981;
Best Local Similarity 99.7%; Pred. No. 2.5e-85;
Matches 333: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 534 CTGCAGAGATGAAAAAGGCCCTCTGATACCTCAAGTTAGTTTACCTTTAAAGAGG 593
DB 1 CTGCAGAGATGAAAAAGGCCCTCTGATACCTCAAGTTAGTTTACCTTTAAAGAGG 60

QY 594 TCGGAAGTAAAGACGCAAGCCTTTCCCGAGCTGGGAAAGGCAACGTCCTTCATG 653
DB 61 TCGGAAGTAAAGACGCAAGCCTTTCCCGAGCTGGGAAAGGCAACGTCCTTCATG 120

QY 654 GCCGGAATGGAACCTTAATTTCCCGTTCCCGCAACGAGCCCGCGAGAGTACTC 713
DB 121 GCCGGAATGGAACCTTAATTTCCCGTTCCCGCAACGAGCCCGCGAGAGTACTC 180

QY 714 TCACGAGACCCGCGAGAGTCAGCTTGGCAATCCGTCGGCGCGCTCCCTTTAT 773
DB 181 TCACGAGACCCGCGAGAGTCAGCTTGGCAATCCGTCGGCGCGCTCCCTTTAT 240

QY 774 AAGCCGACTCGCCCGGCAACGCGAGCGGTTGGGAGGTTGGCTTGGAGGGGTGGTGC 833
DB 241 AAGCCGACTCGCCCGGCAACGCGAGCGGTTGGGAGGTTGGGAGGGGTGGTGC 300

QY 834 CATTTTGTCTTAACCTTAACCTTAACCTTAACCTTAACCTTAACCTTAACCTTA 867
DB 301 CATTTTGTCTTAACCTTAACCTTAACCTTAACCTTAACCTTAACCTTAACCTTA 334

RESULT 14
A84591

LOCUS A84591 981 bp DNA linear PAT 21-JAN-2000
DEFINITION Sequence 1 from Patent WO9845450.
ACCESSION A84591
VERSION A84591.1 GI:6733507
KEYWORDS
SOURCE .
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 981)
AUTHORS Atkinson,E.M. and Kealey,J.T.
TITLE PURIFIED TELOMERASE
JOURNAL Patent: WO 9845450-A 1 15-OCT-1998;
GERON CORP (US)

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source Location/Qualifiers
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/organism="unidentified"
/db_xref="taxon:32644"
misc_RNA .
267..716
/product="HTR"
/note="RNA COMPONENT OF HUMAN TELOMERASE (HTR)"

BASE COUNT 172 a 303 c 305 g 200 t 1 others
ORIGIN

Query Match 38.3%; Score 332.4; DB 6; Length 981;
Best Local Similarity 99.7%; Pred. No. 3.7e-85;
Matches 333: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 534 CTGCAGAGATGAAAAAGGCCCTCTGATACCTCAAGTTAGTTTACCTTTAAAGAGG 593
DB 1 CTGCAGAGATGAAAAAGGCCCTCTGATACCTCAAGTTAGTTTACCTTTAAAGAGG 60

QY 594 TCGGAAGTAAAGACGCAAGCCTTTCCCGAGCTGGGAAAGGCAACGTCCTTCATG 653
DB 61 TCGGAAGTAAAGACGCAAGCCTTTCCCGAGCTGGGAAAGGCAACGTCCTTCATG 120

QY 654 GCCGGAATGGAACCTTAATTTCCCGTTCCCGCAACGAGCCCGCGAGAGTACTC 713
DB 121 GCCGGAATGGAACCTTAATTTCCCGTTCCCGCAACGAGCCCGCGAGAGTACTC 180

QY 714 TCACGAGACCCGCGAGAGTCAGCTTGGCAATCCGTCGGCGCGCTCCCTTTAT 773
DB 181 TCACGAGACCCGCGAGAGTCAGCTTGGCAATCCGTCGGCGCGCTCCCTTTAT 240

QY 774 AAGCCGACTCGCCCGGCAACGCGAGCGGTTGGGAGGTTGGCTTGGAGGGGTGGTGC 833
DB 241 AAGCCGACTCGCCCGGCAACGCGAGCGGTTGGGAGGTTGGGAGGGGTGGTGC 300

QY 834 CATTTTGTCTTAACCTTAACCTTAACCTTAACCTTAACCTTAACCTTAACCTTA 867
DB 301 CATTTTGTCTTAACCTTAACCTTAACCTTAACCTTAACCTTAACCTTAACCTTA 334

RESULT 15
AR063825

LOCUS AR063825 981 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 1 from patent US 5846723.

DB 121 GCCGGAATGGAACCTTAATTTCCCGTTCCCGCAACGAGCCCGCGAGAGTACTC 180

QY 714 TCACGAGACCCGCGAGAGTCAGCTTGGCAATCCGTCGGCGCGCTCCCTTTAT 773

DB 181 TCACGAGACCCGCGAGAGTCAGCTTGGCAATCCGTCGGCGCGCTCCCTTTAT 240

QY 774 AAGCCGACTCGCCCGGCAACGCGAGCGGTTGGGAGGTTGGCTTGGAGGGGTGGTGC 833

DB 241 AAGCCGACTCGCCCGGCAACGCGAGCGGTTGGGAGGTTGGGAGGGGTGGTGC 300

QY 834 CATTTTGTCTTAACCTTAACCTTAACCTTAACCTTAACCTTAACCTTAACCTTA 867

DB 301 CATTTTGTCTTAACCTTAACCTTAACCTTAACCTTAACCTTAACCTTAACCTTA 334

RESULT 14
A84591

LOCUS A84591 981 bp DNA linear PAT 21-JAN-2000

DEFINITION Sequence 1 from Patent WO9845450.

ACCESSION A84591

VERSION A84591.1 GI:6733507

KEYWORDS

SOURCE .

ORGANISM unidentified.

REFERENCE 1 (bases 1 to 981)

AUTHORS Atkinson,E.M. and Kealey,J.T.

TITLE PURIFIED TELOMERASE

JOURNAL Patent: WO 9845450-A 1 15-OCT-1998;

GERON CORP (US)

FEATURES

source Location/Qualifiers

1..981

/organism="unidentified"

/db_xref="taxon:32644"

misc_RNA

267..716

/product="HTR"

/note="RNA COMPONENT OF HUMAN TELOMERASE (HTR)"

BASE COUNT 172 a 303 c 305 g 200 t 1 others

ORIGIN

Query Match 38.3%; Score 332.4; DB 6; Length 981;

Best Local Similarity 99.7%; Pred. No. 3.7e-85;

Matches 333: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 534 CTGCAGAGATGAAAAAGGCCCTCTGATACCTCAAGTTAGTTTACCTTTAAAGAGG 593

DB 1 CTGCAGAGATGAAAAAGGCCCTCTGATACCTCAAGTTAGTTTACCTTTAAAGAGG 60

QY 594 TCGGAAGTAAAGACGCAAGCCTTTCCCGAGCTGGGAAAGGCAACGTCCTTCATG 653

DB 61 TCGGAAGTAAAGACGCAAGCCTTTCCCGAGCTGGGAAAGGCAACGTCCTTCATG 120

QY 654 GCCGGAATGGAACCTTAATTTCCCGTTCCCGCAACGAGCCCGCGAGAGTACTC 713

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QY 714 TCACGAGACCCGCGAGAGTCAGCTTGGCAATCCGTCGGCGCGCTCCCTTTAT 773

DB 181 TCACGAGACCCGCGAGAGTCAGCTTGGCAATCCGTCGGCGCGCTCCCTTTAT 240

QY 774 AAGCCGACTCGCCCGGCAACGCGAGCGGTTGGGAGGTTGGCTTGGAGGGGTGGTGC 833

DB 241 AAGCCGACTCGCCCGGCAACGCGAGCGGTTGGGAGGTTGGGAGGGGTGGTGC 300

QY 834 CATTTTGTCTTAACCTTAACCTTAACCTTAACCTTAACCTTAACCTTAACCTTA 867

DB 301 CATTTTGTCTTAACCTTAACCTTAACCTTAACCTTAACCTTAACCTTAACCTTA 334

RESULT 15
AR063825

LOCUS AR063825 981 bp DNA linear PAT 29-SEP-1999

DEFINITION Sequence 1 from patent US 5846723.

ACCESSION AR063825
VERSION AR063825.1 GI:5993133
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 981)
TITLE Kim,N.Woo., Wu,F., Kealey,J.T., Pruzan,R. and Weinrich,S.L.
JOURNAL Methods for detecting the RNA component of telomerase
FEATURES Patent: US 5846723-A 1 08-DEC-1998;
Location/Qualifiers
source 1..981
/organism="unknown"
BASE COUNT 172 a 303 c 305 g 200 t 1 others
ORIGIN
Query Match 38.3%; Score 332.4; DB 6; Length 981;
Best Local Similarity 99.7%; Pred. No. 3.7e-85;
Matches 333; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 534 CTCGAGAGATAGAAAAAGCCCTGATACCTCAAGTTAGTTTACCTTAAGAAG 593
DB 1 CTCGAGAGATAGAAAAAGWCCCTCTGATACCTCAAGTTAGTTTCACTTAAGAAG 60
QY 594 TCGGAAGTAAAGACGAAAGCCTTTCCGAGCGTGGGAAGGCAACGTCTTCATG 653
DB 61 TCGGAAGTAAAGACGAAAGCCTTTCCGAGCGTGGGAAGGCAACGTCTTCATG 120
QY 654 GCGGAAATGGACTTTAATTTCCCGTTCCCGCAACAGCCCGCCGAGAGAGTACTC 713
DB 121 GCGGAAATGGACTTTAATTTCCCGTTCCCGCAACAGCCCGCCGAGAGTACTC 180
QY 714 TCACGAGAGCCGAGAGTACGCTTGCCCATCGGTGCGGCGCGCCCTTTAT 773
DB 181 TCACGAGAGCCGAGAGTACGCTTGCCCATCGGTGCGGCGCGCCCTTTAT 240
QY 774 AAGCCGACTGCCCGGAGCGCACCGGGTTGCGGAGGGTGGCCGGAAGGGTGGGC 833
DB 241 AAGCCGACTGCCCGGAGCGCACCGGGTTGCGGAGGGTGGCCGGAAGGGTGGGC 300
QY 834 CATTTTTGCTAACCTTAAGTGAAGGCGTA 867
DB 301 CATTTTTGCTAACCTTAAGTGAAGGCGTA 334

Search completed: January 25, 2003, 15:53:38
Job time : 3242 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 25, 2003, 13:41:55 : Search time 303 Seconds
(without alignments)
6443.837 Million cell updates/sec

Title: US-09-601-267-36

Perfect score: 867

Sequence: 1 agctactcagagagctgaga.....ccctactcagagagagcgta 867

Scoring table:

IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	867	100.0	867	AAZ07250	Human telomerase R
2	867	100.0	1765	AAZ07247	Human telomerase R
3	848.6	97.9	2426	AAV22994	DNA containing hum
4	834.6	96.3	2425	AAI10283	Gene for RNA compo
5	834.6	96.3	2425	AAI1027	DNA encoding the h
6	334	38.5	981	AAV41194	PSI1 fragment cont
7	334	38.5	981	AAV19481	Human telomerase h
8	333	38.4	980	AA509471	Human DNA containi
9	333	38.4	981	AAZ24234	Human telomerase (

10	332.4	38.3	981	18	AAI89242	Clone containing h
11	332.4	38.3	981	19	AAV63644	Human telomerase R
12	332.4	38.3	981	20	AAZ23626	Human clone 28-1 c
13	332.4	38.3	981	21	AAI37564	Human telomerase n
14	332.4	38.3	981	23	AAI15442	PSI1 fragment cont
15	176	20.3	176	20	AAZ07323	Human telomerase R
16	176	20.3	176	20	AAZ07251	Human telomerase R
17	155	17.9	680	18	AAI58803	Human telomerase e
18	106	12.2	15650	22	ABAI5903	Human nervous syst
19	106	12.2	15650	22	ABAI5364	Human nervous syst
20	106	12.2	42738	22	AAK68992	Human immune/haema
21	104.8	12.1	26928	22	ABA82620	Human HBW gene reg
22	104.8	12.1	26928	24	ABK22779	Human high bone ma
23	104.4	12.0	20245	22	AAK72318	Human immune/haema
24	104.4	12.0	20245	24	ABK69845	Human immune/haema
25	104.4	12.0	84607	20	AAI90847	Human PKAP genom
26	104.4	12.0	220895	24	ABK84798	Human cDNA differe
27	104	12.0	32134	22	AAI07813	Human cDNA differe
28	104	12.0	32134	22	AAI03615	Human reproductive
29	104	12.0	32191	22	ABA07814	Human reproductive
30	104	12.0	32191	22	AAI03616	Human ovarian and
31	102.8	11.9	15810	24	AAI68995	Human reproductive
32	102.8	11.9	22465	22	AAK86932	Human immune/haema
33	102.8	11.9	44100	21	ABN97975	Human retroviral s
34	102.8	11.9	56093	24	ABL61744	Colon adenocarcino
35	102.6	11.8	5121	22	AAK83937	Human immune/haema
36	102.6	11.8	31853	22	AAI98993	Human excretory re
37	102.6	11.8	31853	22	AAI63343	Human kidney relat
38	102	11.8	18564	22	AAK65368	Human immune/haema
39	101.8	11.7	23544	22	AAI05829	Human reproductive
40	101.8	11.7	23544	23	ABL98393	Human testicular a
41	101.6	11.7	421	23	ABV17393	Human prostate exp
42	101.6	11.7	480	23	ABV47188	Human prostate exp
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44	101.4	11.7	177	21	AAI12382	Human secreted pro
45	101.2	11.7	405	23	ABV49060	Human prostate exp

ALIGNMENTS

RESULT 1	
AAZ07250	AAZ07250 standard; DNA; 867 BP.
ID	AAZ07250
AC	AAZ07250;
XX	
DT	22-OCT-1999 (first entry)
DE	
XX	
DE	Human telomerase RNA gene (hTR) 5' flanking region.
XX	
KW	Telomerase RNA; TR; promoter; cytotoxin; cancer; neoplasia; hTR;
KW	gene therapy; thymidine kinase gene; anticancer therapy; human; ss.
OS	Homo sapiens.
XX	
PN	MO9938964-A2.
XX	
PD	05-AUG-1999.
XX	
PF	29-JAN-1999; 99WO-GB00308.
XX	
PR	29-JAN-1998; 98GB-0001902.
XX	
PA	(CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
XX	
PI	Keith WN;
XX	
DR	WPI: 1999-479183/40.
XX	
PT	Mouse and human telomerase RNA gene promoters, useful for tumor
PT	specific gene therapy
XX	

Claim 3; Fig 4a; 109pp; English.

The invention relates to promoter regions from mouse and human telomerase RNA (TR) component genes. The TR gene promoter can be linked to a heterologous gene, especially a gene encoding a cytotoxin, for therapy of cancer, especially neoplasias. The telomerase is necessary for the unrestricted proliferative capacity of many human cancers. Mutation or dysregulation of the telomerase expression pathway may cause reactivation or upregulation of telomerase expression in cancer. Substances, identified in the methods can be used to block transcription from the TR gene promoter through interaction of the 5' regulatory sequences. These substances, e.g. antisense oligonucleotides, transcription factors, peptide nucleic acids and factors that disrupt signal transduction, are useful for cancer therapy. In particular, gene therapy vectors (especially poB7-codAmp) comprising the promoter and a viral thymidine kinase gene can be used to convert a prodrug, e.g. gancyclovir, so that neoplasia can be controlled or treated. Direct down-regulation of telomerase RNA gene through manipulation of transcription factors may be effective anticancer therapy and the cloning of the hTR gene promoter allows the analysis of therapeutic molecules which modulate hTR promoter activity. The present sequence represents a human TR gene (htrf) 5' flanking sequence.

Sequence 867 BP; 237 A; 209 C; 221 G; 200 T; 0 other;

Query match	100.08;	Score 867;	DB 20;	Length 867;
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Best Local Similarity 100.0%; Pred. No. 3.7e-268;

Matches 867; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY	61	AGCGAGATCAAGCCACTAGACTCCATCCACGCTTGAGGCGAAGAGCAAGCTCCGTCTCA	120
Db	61	AGCGAGATCAAGCCACTAGACTCCATCCACGCTTGAGGCGAAGAGCAAGCTCCGTCTCA	120
OY	121	AAAAAAAAATTCGTTACATTTATGGTGGATTACTCCCTCTTTTAACTTCATCAGACA	180
Db	121	AAAAAAAAATTCGTTACATTTATGGTGGATTACTCCCTCTTTTAACTTCATCAGACA	180
OY	181	CAGCACTACTTTAAAGCAAGATCAATGTGAAGAGGCTTTGCTTCTTAAATAAAGGAG	240
Db	181	CAGCACTACTTTAAAGCAAGATCAATGTGAAGAGGCTTTGCTTCTTAAATAAAGGAG	240
OY	241	ATTCAGTCTTAAAGTAAATATATGTAGTAGTTACACTTGATTAAGCCATCCTCTGCTCA	300
Db	241	ATTCAGTCTTAAAGTAAATATATGTAGTAGTTACACTTGATTAAGCCATCCTCTGCTCA	300
OY	301	AGGGAAGCTGTGGAAGGCAATCTTAAGSAAAAAGGGCAGGGTTGGAACTCGACGATC	360
Db	301	AGGGAAGCTGTGGAAGGCAATCTTAAGSAAAAAGGGCAGGGTTGGAACTCGACGATC	360
OY	361	CCACTGAGCCGAGACAAGATTCTCTGTAGCACTGCGCTGGGAATCTAATTTTCACAA	420
Db	361	CCACTGAGCCGAGACAAGATTCTCTGTAGCACTGCGCTGGGAATCTAATTTTCACAA	420
OY	421	AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAAGTTCGTGTGCTTAGGCCCTA	480
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Db	541	GGATAGAAAAAGACCCCTGTGATACCTCAAGTTAGTTTACCTTTAAAGAAAGTCCGAAG	600
OY	601	TAAAGACGCAAGCCCTTTCCGGACGTGCGGAAGGCAAGCTCCTTCATGAGCGGAA	660
Db	601	TAAAGACGCAAGCCCTTTCCGGACGTGCGGAAGGCAAGCTCCTTCATGAGCGGAA	660

QY	661	ATGAAACCTTAAATTTCCCGTTCCCGCCCAACAGCCGCCCGGAGAGAGTACTCTCAGAC	720
Db	661	ATGGAACCTTAAATTTCCCGTTCCCGCCCAACAGCCGCCCGGAGAGTACTCTCAGAC	720
QY	721	AGCCCGAGAGTCAAGCTTGGCCATCCGTGGCGTCCGCGCCGCTCCCTTATTAAGCCGA	780
Db	721	AGCCCGAGAGTCAAGCTTGGCCATCCGTGGCGTCCGCGCCGCTCCCTTATTAAGCCGA	780
QY	781	CTCGCCCGGACGACCGGGTTGCGAGAGGTGGGCCCTGGAGAGGCTGATGGCCATTTTTT	840
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QY	841	TGTCTAACCTTAAGAGAGGGCGTGA	867
Db	841	TGTCTAACCTTAAGAGAGGGCGTGA	867

RESULT 2

ID AAZ07247 standard; DNA; 1765 BP.

AC AAZ07247;

DT 22-OCT-1999 (first entry)

Human telomerase RNA (hTR) gene sequence

KW Telomerase RNA; TR; promoter; cytotoxin; cancer; neoplasia; hTR;

KW gene therapy; thymidine kinase gene; anticancer therapy; human; ss.

OS Homo sapiens.

PN W09938964-A2.

PD 05-AUG-1999

PF 29-JAN-1999; 99WO-GB00308

PR 29-JAN-1998; 98GB-0001902.

PA (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.

PI Keith WN;

DR WPI; 1999-479183/40.

PT Mouse and human telomerase RNA gene promoters, useful for tumor

XX

CC The invitation relates to promote the regions from cause and human telomerase
CC RNA (TR) component genes. The TR gene promoter can be linked to a
CC heterologous gene, especially a gene encoding a cytotoxin, for therapy
CC of cancer, especially neoplasias. The telomerase is necessary for the
CC unrestricted proliferative capacity of many human cancers. Mutation or
CC dysregulation of the telomerase repression pathway may cause reactivation
CC or upregulation of telomerase expression in cancer. Substances,
CC identified in the methods can be used to block transcription from the TR
CC gene promoter through interaction of the 5' regulatory sequences. These
CC substances, e.g. antisense oligonucleotides, transcription factors,
CC useful for nucleic acids and factors that disrupt signal transduction, are
CC specific for cancer therapy. In particular, gene therapy vectors
CC (especially pG62-codanup) comprising the promoter and a viral thymidine
CC kinase gene can be used to convert a prodrug, e.g. gancyclovir, so that
CC neoplasia can be controlled or treated. Direct down-regulation of
CC telomerase RNA gene through manipulation of transcription factors may be
CC effective anticancer therapy and the cloning of the hTR gene promoter
CC allows the analysis of therapeutic molecules which modulate hTR promoter
CC activity. The present sequence represents a human TR (hTR) gene sequence.

SQ Sequence 1765 BP; 404 A; 458 C; 480 G; 423 T; 0 other;


```

Query Match          100.0%; Score 867; DB 20; Length 1765;
Best Local Similarity 100.0%; Pred. No. 5,5e-268;
Matches 867; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTACTCAGGAGGCTGAGACACGAGAAATCGCTTGAACCCGGGAGGACAGAGTTGCAGTG 60
   |||||
DB 1 ACTTACTCAGGAGGCTGAGACACGAGAAATCGCTTGAACCCGGGAGGACAGAGTTGCAGTG 60

QY 61 AGCCGAGATCAGGCGGCTGATCCATCCAGCGCTGGGCGAAAGAGCAACATCCGCTCA 120
   |||||
DB 61 AGCCGAGATCAGGCGGCTGATCCATCCAGCGCTGGGCGAAAGAGCAACATCCGCTCA 120

QY 121 AAAAAAAAAATCGTTACAAATTTATGGTGGATTACTCCCTCTTTTACCTCATCAGACA 180
   |||||
DB 121 AAAAAAAAAATCGTTACAAATTTATGGTGGATTACTCCCTCTTTTACCTCATCAGACA 180

QY 181 CAGCACTACTTTTAAGCAAAAGTCATGATTGAACGCCCTTTCTTCTTAATAAAGGAG 240
   |||||
DB 181 CAGCACTACTTTTAAGCAAAAGTCATGATTGAACGCCCTTTCTTCTTAATAAAGGAG 240

QY 241 ATTCACTCCTTAAGATTATTAATGTAGTAACTGATTAACCAATCCCTGCTCA 300
   |||||
DB 241 ATTCACTCCTTAAGATTATTAATGTAGTAACTGATTAACCAATCCCTGCTCA 300

QY 301 AGGAGAACTGGAGAGAGCATTTCTAAGAAAAAGGGGAGGTTGGAACTCGAGCATC 360
   |||||
DB 301 AGGAGAACTGGAGAGAGCATTTCTAAGAAAAAGGGGAGGTTGGAACTCGAGCATC 360

QY 361 CCACGTGAGCCGAGACAAAGATTCTGCTGATGACAGTCTGCGGAATCTATTTTCACA 420
   |||||
DB 361 CCACGTGAGCCGAGACAAAGATTCTGCTGATGACAGTCTGCGGAATCTATTTTCACA 420

QY 421 AGTTCTCCAAAAATGTGATCAAAACTAGGAATTAAGTTCCTGCTCTAAGGCCCTA 480
   |||||
DB 421 AGTTCTCCAAAAATGTGATCAAAACTAGGAATTAAGTTCCTGCTCTAAGGCCCTA 480

QY 481 AATCTTCTCTGTAATTCATTTTAAAGTAGTCAGAGTGAACCGGCTGCTGCTCAGA 540
   |||||
DB 481 AATCTTCTCTGTAATTCATTTTAAAGTAGTCAGAGTGAACCGGCTGCTGCTCAGA 540

QY 541 GGATAGAAAAAGGCGCTGTGATACCTCAAGTTCACCTTTAAAGAGGTCGGAAG 600
   |||||
DB 541 GGATAGAAAAAGGCGCTGTGATACCTCAAGTTCACCTTTAAAGAGGTCGGAAG 600

QY 601 TAAAGACGCAAAAGCCTTCCGGAAGTGGGGAAGGCAACGTCCTTCATGCGCGGA 660
   |||||
DB 601 TAAAGACGCAAAAGCCTTCCGGAAGTGGGGAAGGCAACGTCCTTCATGCGCGGA 660

QY 661 ATGGAACCTTAAATTTCCGTTCCCGCCCAACAGCCCGCCGAGAGAGTACTCTACGAG 720
   |||||
DB 661 ATGGAACCTTAAATTTCCGTTCCCGCCCAACAGCCCGCCGAGAGAGTACTCTACGAG 720

QY 721 AGCCGAGAGATCAGCTTGGCAATCCGTCGGGTCGGCGCTCCCTTTATAGCCGA 780
   |||||
DB 721 AGCCGAGAGATCAGCTTGGCAATCCGTCGGGTCGGCGCTCCCTTTATAGCCGA 780

QY 781 CTTGCGCCGCGACGCGACCGGTTGGGAGGCTGGGCTGGAGGGGTGGTGGCCATTTT 840
   |||||
DB 781 CTTGCGCCGCGACGCGACCGGTTGGGAGGCTGGGCTGGAGGGGTGGTGGCCATTTT 840

QY 841 TGTCTTAACCTTAACCTGAGAGAGGCGCTA 867
   |||||
DB 841 TGTCTTAACCTTAACCTGAGAGAGGCGCTA 867

RESULT 3
AAV22994 standard: DNA; 2426 BP.
XX
AC AAV22994:
XX
DT 30-JUL-1998 (first entry)
XX

```

```

DE DNA containing human telomerase RNA component gene sequences.
XX
KW Human; telomerase RNA component gene sequence;
KW Ribonucleoprotein enzyme; cancer cell; telomerase activity;
KW reporter construct; transcription regulatory region;
KW prophylaxis; therapy; telomerase-related condition;
KW chromatin position effect; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT TATA_signal 1438..1444
FT /tag= a
FT misc_feature 1238..1259
FT /tag= b
FT /note= "PSE consensus sequence"
FT /tag= c
FT /note= "PSE consensus sequence"
FT /note= "PSE consensus sequence"
FT CAAT_signal 1399..1406
FT /tag= d
FT misc_feature 1354..1359
FT /tag= e
FT /note= "SPl consensus sequence"
FT /tag= f
FT /note= "beta-interferon response element"
XX
XX WO9811207-A2.
XX
XX 19-MAR-1998.
XX
XX 16-SEP-1997; 97WO-US16450.
XX
XX 16-SEP-1996; 96US-0714482.
XX
XX (GERO-) GERON CORP.
XX
XX Harley C, Villeponteau B;
XX
XX WPI; 1998-207376/18.
XX
XX Human telomerase reporter constructs - useful in assays for
XX regulators of mammalian telomerase expression
XX
XX Claim 6; Pages 27-28; 59pp; English.
XX
XX The present sequence contains human telomerase RNA component gene
XX sequences. Telomerase is a ribonucleoprotein enzyme that synthesizes
XX one strand of the telomeric DNA using as a template a sequence contained
XX within the RNA component of the enzyme. Most cancer cells express high
XX levels of telomerase activity, while in normal somatic human cells,
XX telomerase is not detected. The specification describes the production
XX of a telomerase reporter construct which comprises a recombinant
XX polynucleotide having a transcription regulatory region of a telomerase
XX gene operably linked to a nucleotide sequence encoding a reporter
XX polynucleotide heterologous to the transcription regulatory region.
XX Expression of the reporter polynucleotide is detectable. The telomerase
XX reporter construct is used in screening assays for determining modulators
XX of transcription. The modulators can be used for prophylaxis or therapy
XX of telomerase-related conditions. The reporter construct which has a
XX selectable drug marker can be used to generate position effect reporter
XX cells which can be used to determine whether a test agent inhibits
XX chromatin position effect. Tagged RNA component constructs can be used
XX to determine whether an agent modulates association between a mammalian
XX RNA telomerase component and a mammalian telomerase.
XX
XX Sequence 2426 BP; 620 A; 575 C; 650 G; 581 T; 0 other;

```

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Query Match          97.9%; Score 848.6; DB 19; Length 2426;
Best Local Similarity 99.4%; Pred. No. 5,5e-262;
Matches 862; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

```

OY	1	AGTACTCAGGAGGCTCAGACACGAGAAATGCTTTGAACCCGGGAGGCGAGAGTTGCACTG	60
Dp	662	AGCTACTCAGGAGGCTCAGACACGAGAAATGCTTTGAACCCGGGAGGCGAGAGTTGCACTG	720
OY	61	AGCGAGATCAGCGCAGTAACTCCATCCAGCCTGGGGCAAGAGCAAGATCCGTCGA	120
Dp	721	AGCGAGATCAGCGCAGTAACTCCATCCAGCCTGGGGCAAGAGCAAGATCCGTCGA	780
OY	121	AAAAAAAAATCGTTACAAATTTATGGTGAATTAAGTGAAGGCGCTTCCTTCCTAATAAAGGAG	180
Dp	781	AAAAAAAAATCGTTACAAATTTATGGTGAATTAAGTGAAGGCGCTTCCTTCCTAATAAAGGAG	840
OY	181	CAGAGACTCTTAAAGCAAGTCATGATGGAAGGCGCTTCCTTCCTAATAAAGGAG	240
Dp	841	CAGAGACTCTTAAAGCAAGTCATGATGGAAGGCGCTTCCTTCCTAATAAAGGAG	900
OY	241	ATTGAGTCCTTAAGATTAATATGATAGTATACACTTGATTAAGGCAATCCCTGCTGCA	300
Dp	901	ATTGAGTCCTTAAGATTAATATGATAGTATACACTTGATTAAGGCAATCCCTGCTGCA	960
OY	301	AGGAGAACTTGGAGAAAGGCAATTTAAAGAAAAGGGGCAAGGTTGGAACTCGGACGCATC	360
Dp	961	AGGAGAACTTGGAGAAAGGCAATTTAAAGAAAAGGGGCAAGGTTGGAACTCGGACGCATC	1020
OY	361	CCACTGAGCGGAGACAAGATTCGTGTAGTCACTGCTCCCTGGGAAATCTATTTTCAACA	420
Dp	1021	CCACTGAGCGGAGACAAGATTCGTGTAGTCACTGCTCCCTGGGAAATCTATTTTCAACA	1080
OY	421	AGTTCTCCAAAAAATGATGATCAAAACCTAGGAATTAAGTGTGTGTCTTAAAGGCGCTA	480
Dp	1081	AGTTCTCCAAAAAATGATGATCAAAACCTAGGAATTAAGTGTGTGTCTTAAAGGCGCTA	1140
OY	481	AAATCTTCAGTGAATCCATTTTAAAGGAGTGCAGAGTGAACCCGCTCGTCGACGA	540
Dp	1141	AAATCTTCAGTGAATCCATTTTAAAGGAGTGCAGAGTGAACCCGCTCGTCGACGA	1200
OY	541	GGATAGAAAAAGGCGCTCTGATACCTCAAGTTAGTTTACCTTTAAAGAAAGTCTGAG	600
Dp	1201	GGATAGAAAAAGGCGCTCTGATACCTCAAGTTAGTTTACCTTTAAAGAAAGTCTGAG	1260
OY	601	TAAAGACGCAAAAGCTTTCCCGGAGCTGGGGAAAGGCAACGTCCTTCCTATGGCGGAA	660
Dp	1261	TAAAGACGCAAAAGCTTTCCCGGAGCTGGGGAAAGGCAACGTCCTTCCTATGGCGGAA	1320
OY	661	ATGGAACCTTAATTTCCCGTTCGCCCAACCAAGCCGCGCGAGAGATGACTCTACAG	720
Dp	1321	ATGGAACCTTAATTTCCCGTTCGCCCAACCAAGCCGCGCGAGAGATGACTCTACAG	1380
OY	721	AGCGCGAGAGTCAAGCTTTGGCCCAATCCGTCGCGTGGCGGCGCGCTTCCTTTAAGCCGA	780
Dp	1381	AGCGCGAGAGTCAAGCTTTGGCCCAATCCGTCGCGTGGCGGCGCGCTTCCTTTAAGCCGA	1440
OY	781	CTCCCGCGGAGCGCAACCGGTTGCGGAGGAGTGGGCTTGGAGGGGTGTGGCCATTTT	840
Dp	1441	CTCCCGCGGAGCGCAACCGGTTGCGGAGGAGTGGGCTTGGAGGGGTGTGGCCATTTT	1500
OY	841	TGTCTAACCTTAAGTGAAGGCGCTGA	867
Dp	1501	TGTCTAACCTTAAGTGAAGGCGCTGA	1527

RESULT 4
AAT10283
ID AAT10283 standard; DNA; 2425 BP.
XX
XX AAT10283; 1
XX
DT 09-SEP-1996 (first entry)
XX
DE Gene for RNA component of human telomerase.
XX
XX RNA component; human; telomerase; lung fibroblast; cell line WI-38.
KW recombinant production; synthesis; mutant; detection; mammalian.

KW	identification; modulating agent; neoplastic condition; gene;
KM	transcriptional regulatory sequence; gene therapy; disease; ss.
XX	
OS	Homo sapiens.
XX	
PN	W09601835-A1.
XX	
PD	25-JAN-1996.
XX	
PF	06-JUL-1995; 95WO-US08530.
XX	
PR	07-JUN-1995; 95US-0482115.
PR	07-JUL-1994; 94US-0272102.
PR	27-OCT-1984; 94US-0330123.
PR	07-JUN-1995; 95US-0472802.
XX	
PA	(GERO-) GERON CORP.
XX	
PI	Andrews WH, Feng J, Funk W, Villeponteau B;
XX	
DR	WPI; 1996-097581/10.
XX	
PT	RNA component of mammalian telomerase, esp. human - useful in
PT	identifying e.g. candidate telomerase-modulating agents
XX	
PS	Claim 14; Pages 97-98; 114pp; English.

Claim 14; Pages 97-98; 114pp; English.

The present sequence is the gene for the RNA component of human telomerase (RCHT), which was derived from a genomic DNA library obtd. from the human lung fibroblast cell line WI-38. The gene and the RCHT can be used in the recombinant prodn. of an active telomerase mol., capable of adding sequences to chromosomal DNA telomeres, and in the synthesis of mutant sequences for the detection of mutant mammalian telomerase RNA component polynucleotides. The RCHT may also be used in the identification of telomerase modulating agents, and in the detection of telomerase related or neoplastic conditions in a patient. Polynucleotides of at least 25 consecutive nucleotides identical or complementary to the RCHT sequence linked to heterologous transcriptional regulatory sequences, can be used for the gene therapy of human diseases.

transcriptional regulatory sequences, can be used for the gene therapy of human diseases.

Sequence 2425 BP; 622 A; 572 C; 650 G; 581 T; 0 other;

Query Match	96.38;	Score 834.6;	DB 17;	Length 2425;
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Matches 862; Conservative 0; Mismatches 4; Indels 5; Gaps 2;

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Statistics	Conservative	Mismatches	Indels	Gaps
862;	0;	4;	5;	2;

QY	1	AGTACTCAGGAGGCTGAGACAGAGAAATTCGTTGAACCCGGGAGGCAAGAGTTTGCAATG	60
Db	662	AGCTACTCAGGAGGCTGAGACAGAAATTCGTTGAACCCGGGAGGCAAGAGTTTGCAATG	720
QY	61	AGCCGAAATCAGCCACACTTAACCTCCATTCACAGCCTGGGGCAAGAGACAGACTCGCTTCA	120
Db	721	AGCCGAAATCAGCCACACTTAACCTCCATTCACAGCCTGGGGCAAGAGACAGACTCGCTTCA	780
QY	121	AAAAAAAAATCGTTACAAATTTATGGTGGATTACTCCCTCTTTTACCCTCATCAAGACA	180
Db	781	AAAAAAAAATCGTTACAAATTTATGGTGGATTACTCCCTCTTTTACCCTCATCAAGACA	840
QY	181	CAGACACTACTTTAAAGCAAAAGTCATGATTGAACGCCCTTCTTTCTTAATTAAGAAGSAG	240
Db	841	CAGACACTACTTTAAAGCAAAAGTCATGATTGAACGCCCTTCTTTCTTAATTAAGAAGSAG	900
QY	241	ATTTCAGTCCTTAAGATTAAATATGATGATGTTACACTTGATTAAGCCATCTCTGCTCA	300
Db	901	ATTTCAGTCCTTAAGATTAAATATGATGATGTTACACTTGATTAAGCCATCTCTGCTCA	960
QY	301	AGGAGAGCTGGAGAAAGGCATTCCTTAAGAAAAAGGGGCAAGGTTGCACTGGAGCGCATC	360
Db	961	AGGAGAGCTGGAGAAAGGCATTCCTTAAGAAAAAGGGGCAAGGTTGCACTGGAGCGCATC	1020
QY	361	CCACTGAGCCGAGACAAAGATTCTGCTGATAGTACAGTGTGCTCCCTGGGAAATCTATTTTCAACA	420

361 CCACTGAGCCGAGACAGAATTCTGCTGTAGTCAGTGCCTGCCCTGGGAATCTATTTTCA
420


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|||||
Db 1441 CTCGCCGCGAGCGACCGGTTGCGAGGAGGCGGTGCGAGGCGGTGGCCAT 1500
OY 837 TTTTGTCTAACCTACTGAGAGGCGCTA 867
Db 1501 TTTTGTCTAACCTACTGAGAGGCGCTA 1531

RESULT 6
AAV41194
ID AAV41194 standard; DNA; 981 BP.
XX
AC AAV41194:
XX
DT 08-OCT-1998 (first entry)
XX
DE PstI fragment containing RNA component of human telomerase (hTR).
XX
KW RNA component; human telomerase; antisense oligonucleotide; infection;
KW neuroblastoma; bladder cancer; colon cancer; prostate cancer; cancer;
KW contraception; sterilisation; immunosuppression; therapeutic; hTR;
KW immune system down-regulation; anti-inflammatory therapy; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FH misc_feature 266..716
FT /tag= a
FT /note= "RNA component of human telomerase (hTR)"
FT misc_feature 311..320
FT /tag= b
FT /note= "template region of hTR"
XX
PN MO9828442-A1.
XX
PD 02-JUL-1998.
XX
PF 19-DEC-1997; 97WO-US23619.
XX
PR 20-DEC-1996; 96US-0770565.
PR 20-DEC-1996; 96US-0770564.
XX
PA (GERO-) GERON CORP.
XX
PI Kealey JT, Kim NW, Pruzan R, Weinrich SL, Wu F;
PI WPI: 1998-377670/32.
XX
DR New polynucleotide(s) anti:sense to human telomerase - used for
PT detecting or inhibiting human telomerase, e.g. for treating cancers,
PT contraception, immuno-suppression or treating infection
XX
PS Disclosure; Page 53; 80pp; English.
XX
CC This represents a pstI fragment containing the RNA component of human
CC telomerase (hTR). The invention provides antisense oligonucleotides
CC (AAV41169 to AAV41181) to hTR. These antisense oligonucleotides
CC specifically hybridise to a nucleotide sequence within an accessible
CC region of the hTR, but that does not hybridise to a sequence within the
CC template region of hTR. These oligonucleotides may specifically be used
CC for detection of an RNA component of human telomerase in a sample. This
CC is useful for diagnosing cancer (especially neuroblastoma, bladder, colon
CC and prostate cancer), and providing prognosis for a cancer patient. The
CC inhibitory oligonucleotides can inhibit the telomerase activity level in
CC a cell by interfering with transcription of the RNA component, decreasing
CC the half-life of the telomerase RNA component transcript, inhibiting
CC assembly of the RNA component into the telomerase holoenzyme, or
CC inhibiting the polymerase activity of telomerase. These antisense
CC oligonucleotides can be used for inhibiting telomerase activity in both
CC cultured cells and in cells in vivo. They can be used in therapeutics for
CC treating or preventing cancer, for contraception or sterilisation, for
CC immunosuppression, and for selectively down-regulating specific branches
CC of the immune system, e.g. a specific subset of T-cells, in anti-
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CC inflammatory therapies or for treating infections by, e.g. yeast,
CC parasites or fungi.
XX
SQ Sequence 981 BP; 172 A; 303 C; 306 G; 200 T; 0 other;
Query Match 38.5%; Score 334; DB 19; Length 981;
Best Local Similarity 100.0%; Pred. No. 1,1e-96;
Matches 334; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 534 CTCGAGAGCATAGAAAAAGCCCTCTGATACCTCAAGTTAGTTACCTTAAGAAG 593
Db 1 CTCGAGAGATAGAAAAAGCCCTCTGATACCTCAAGTTAGTTACCTTAAGAAG 60
OY 594 TCGGAAGTAAGACGCAAAAGCTTTCCCGAGCTGGGGAAGGCAAGTCCTTCACAG 653
Db 61 TCGGAAGTAAGACGCAAAAGCTTTCCCGAGCTGGGGAAGGCAAGTCCTTCACAG 120
OY 654 GCCGGAATGGAACTTAAATTTCCCGTCCCAACCAAGCCCGCCGAGAGTACTC 713
Db 121 GCCGGAATGGAACTTAAATTTCCCGTCCCAACCAAGCCCGCCGAGAGTACTC 180
OY 714 TCACGAGAGCCCGGAGAGTCAGCTTGCCCAATCCGTGCGGTGGCGCGCTCCCTTAT 773
Db 181 TCACGAGAGCCCGGAGAGTCAGCTTGCCCAATCCGTGCGGTGGCGCGCTCCCTTAT 240
OY 774 AAGCCGACTGCGCCGCGAGCGCAACGGGTTGGGAGGAGTGCGCTGGGAGGCGTGGCG 833
Db 241 AAGCCGACTGCGCCGCGAGCGCAACGGGTTGGGAGGAGTGCGCTGGGAGGCGTGGCG 300
OY 834 CATTTTGTCTAACCTACTGAGAAGGCGCTA 867
Db 301 CATTTTGTCTAACCTACTGAGAAGGCGCTA 334

RESULT 7
AAV19481
ID AAV19481 standard; cDNA; 981 BP.
XX
AC AAV19481:
XX
DT 28-AUG-1998 (first entry)
XX
DE Human telomerase hTR gene.
XX
KW Telomerase; hTR gene; TPC2; TPC3; telomere length; human; cancer;
KW gene therapy; diagnosis; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FH unsure 21
FT /tag= a
FT mRNA 266..715
FT /tag= b
XX
PN MO9811204-A1.
XX
PD 19-MAR-1998.
XX
PF 13-SEP-1996; 96WO-US14679.
XX
PR 13-SEP-1996; 96WO-US14679.
XX
PA (GERO-) GERON CORP.
XX
PI Adams RR, Andrews WH, Feng J, Villeponteau B;
PI WPI: 1998-207373/18.
XX
DR Human TPC2, TPC3 and TR genes - regulate telomere length or modulate
PT telomerase activity
XX
PS Disclosure; Fig 9A-B; 86pp; English.
```

XX This nucleotide sequence comprises an approximately 1 kb psi
CC restriction fragment of plasmid pGRN33 that includes the human
CC telomerase hTR gene. hTR3 mRNA levels correlate with telomerase
CC activity levels in a variety of mortal and immortal cell lines.
CC In methods of the invention, measurements of telomere length,
CC telomerase activity or hTR levels can be used to identify immortal
CC cells, such as cancer cells, and to evaluate the proliferative
CC capacity of the cell. Gene therapy vectors encode useful nucleic
CC acids such as hTR, or antisense nucleic acids or ribozymes that
CC target TERC, TERC3 (see AAV19479-80) and/or hTR gene products.
XX
SQ Sequence 981 BP; 172 A; 303 C; 306 G; 200 T; 0 other;
Query Match 38.5%; Score 334; DB 19; Length 981;
Best Local Similarity 100.0%; Pred. No. 1,1e-96;
Matches 334; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 534 CTGCAGAGATAGAAAAAGCCCTCTGATACCTCAAGTTAGTTGACCTTTAAAGAAG 593
DB 1 CTGCAGAGATAGAAAAAGCCCTCTGATACCTCAAGTTAGTTGACCTTTAAAGAAG 60
QY 594 TCGGAAGTAAAGACGCAAAAGCCTTCCCGACCTGCGGAAGGCGCAACGTCCTTCATG 653
DB 61 TCGGAAGTAAAGACGCAAAAGCCTTCCCGACCTGCGGAAGGCGCAACGTCCTTCATG 120
QY 654 GCCGAAATGGAAGTAAATTTCCGTCCTCCCAACAGCCCGCGAGAGAGTACTC 713
DB 121 GCCGAAATGGAAGTAAATTTCCGTCCTCCCAACAGCCCGCGAGAGAGTACTC 180
QY 714 TCACGAGAGCCCGAGAGTACGTTGGCCCAATCCGTGCGGTCGCGGCTCCCTTAT 773
DB 181 TCACGAGAGCCCGAGAGTACGTTGGCCCAATCCGTGCGGTCGCGGCTCCCTTAT 240
QY 774 AACCCAGCTCGCCGCGAGCGCAACGGGTTGCGAGAGGTCGCGGTCGCGGTCGCGG 833
DB 241 AACCCAGCTCGCCGCGAGCGCAACGGGTTGCGAGAGGTCGCGGTCGCGGTCGCGG 300
QY 834 CATTTTGTCTAACCTTAAGTGAAGGCGTA 867
DB 301 CATTTTGTCTAACCTTAAGTGAAGGCGTA 334
RESULT 8
AAS09471
ID AAS09471 standard; DNA; 980 BP.
XX
AC AAS09471;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human DNA containing the RNA component of telomerase.
XX
KW Human; Telomerase; RNA component; vaccine; antibody; cancer; EF2H;
XX nucleolin; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT misc_feature 21
FT /tag= a
FT /note= "Designated 0 in the specification, with 7
FT in the complementary strand"
FT 311..320
FT /tag= b
FT /label= "Template-region"
FT /note= "This region is not further defined in the
FT specification"
XX
PN US6261556-B1.
XX
PD 17-JUL-2001.
XX

PF 18-OCT-1999; 9905-0420056.
XX
XX 04-APR-1997; 97US-0833377.
PR 04-AUG-1995; 95US-0510736.
XX
PA (GERO-) GERON CORP.
PI Weinrich SL, Atkinson EM, Lichtsteiner SP, Vasserot AP, Pruzan RA;
PI Kealey JT;
XX
DR WPI; 2001-450477/48.
XX
XX Purified human telomerase, useful for inducing immune response in
PT animals, comprises several thousand folds increased purity compared
PT with cytoplasmic crude cell preparations -
XX
PS Disclosure; Column 9-12; 29pp; English.
XX
XX The sequence contains human telomerase, hTR, RNA component. The invention
CC relates to a purified human telomerase core enzyme protein comprising
CC 2000-fold increased purity compared with a crude extract of cells from
CC adenovirus-transformed kidney cell line (293 cells) and when associated
CC with telomerase RNA component has DNA polymerase activity and a molecular
CC weight of 200-2000 Kilo Daltons (KDa). The purified telomerase is useful
CC for inducing a humoral or cell-mediated immune response in an animal.
CC Purified telomerase or immunogenic fragments are useful as vaccines for
CC treating diseases associated with over-expression of telomerase, such as
CC cancer and for producing antibodies that recognize telomerase, which are
CC useful as affinity agents in isolating the proteins and for detecting the
CC presence of proteins in a sample, such as cell or tissue. Identification
CC of telomerase aids in diagnosis of cancer or pre-cancerous states.
CC Telomerase and/or telomerase associated proteins are also useful for
CC screening compounds to identify agents that alter the association of
CC telomerase-associated proteins, such as nucleolin or EF2H with
CC telomerase.
XX
SQ Sequence 980 BP; 171 A; 303 C; 305 G; 200 T; 1 other;
Query Match 38.4%; Score 333; DB 22; Length 980;
Best Local Similarity 99.7%; Pred. No. 2.3e-96;
Matches 333; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 534 CTGCAGAGATAGAAAAAGCCCTCTGATACCTCAAGTTAGTTGACCTTTAAAGAAG 593
DB 1 CTGCAGAGATAGAAAAAGCCCTCTGATACCTCAAGTTAGTTGACCTTTAAAGAAG 60
QY 594 TCGGAAGTAAAGACGCAAAAGCCTTCCCGACCTGCGGAAGGCGCAACGTCCTTCATG 653
DB 61 TCGGAAGTAAAGACGCAAAAGCCTTCCCGACCTGCGGAAGGCGCAACGTCCTTCATG 120
QY 654 GCCGAAATGGAAGTAAATTTCCGTCCTCCCAACAGCCCGCGAGAGAGTACTC 713
DB 121 GCCGAAATGGAAGTAAATTTCCGTCCTCCCAACAGCCCGCGAGAGAGTACTC 180
QY 714 TCACGAGAGCCCGAGAGTACGTTGGCCCAATCCGTGCGGTCGCGGCTCCCTTAT 773
DB 181 TCACGAGAGCCCGAGAGTACGTTGGCCCAATCCGTGCGGTCGCGGCTCCCTTAT 240
QY 774 AACCCAGCTCGCCGCGAGCGCAACGGGTTGCGAGAGGTCGCGGTCGCGGTCGCGG 833
DB 241 AACCCAGCTCGCCGCGAGCGCAACGGGTTGCGAGAGGTCGCGGTCGCGGTCGCGG 300
QY 834 CATTTTGTCTAACCTTAAGTGAAGGCGTA 867
DB 301 CATTTTGTCTAACCTTAAGTGAAGGCGTA 334
RESULT 9
AAD24234
ID AAD24234 standard; DNA; 981 BP.
XX
AC AAD24234;
XX

DT 07-MAR-2002 (first entry)
 XX Human telomerase (htr) gene.
 DE
 XX
 KM Human; telomerase; TR; telomerase activity-related disease; therapy;
 KM cancer; pregnancy; fertility; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT misc_feature 267..715
 FT /*tag= a
 FT /note= "htr transcript serves as template in the
 FT telomerase ribonucleoprotein"
 FT
 PN US6300110-B1.
 XX
 PD 09-OCT-2001.
 XX
 PF 23-DEC-1998; 98US-0220157.
 XX
 PR 09-SEP-1995; 95US-003492P.
 PR 13-SEP-1996; 96US-0710249.
 PR 05-JAN-1996; 96US-0583808.
 XX
 PA (GERO-) GERON CORP.
 XX
 PI VILLEPONTIEU B, FENG J, ANDREWS WH, ADAMS RR;
 XX
 DR WPI; 2002-033174/04.
 XX
 PT Peptide products of the human TPC2 and TPC3 gene are involved in
 PT regulation of telomere length and activity are useful to diagnose and
 PT treat telomere length and activity-related diseases -
 XX
 PS Example; Fig 9; 60pp; English.
 XX
 CC The invention relates to methods and reagents for regulating telomere
 CC length and for modulating telomerase activity in mammalian cells. The
 CC invention also relates to purified, synthetic or recombinant peptides
 CC such as TPC2 or TPC3 used for detecting regulators of telomere length
 CC and telomerase activity in mammalian cells and for a variety of related
 CC diagnostic and therapeutic purposes. The method is useful for screening,
 CC diagnosing, monitoring and treating diseases and other conditions such as
 CC cancer, pregnancy, fertility, telomere length and telomerase-activity.
 CC The present sequence is human telomerase (htr) gene.
 CC
 XX
 SO Sequence 981 BP; 172 A; 303 C; 305 G; 200 T; 1 other;

Query Match 38.4%; Score 333; DB 24; Length 981;
 Best Local Similarity 99.7%; Pred. No. 2.3e-96;
 Matches 333; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 534 CTGCAGAGGATTAAGAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACTTTAAAGAGG 533
 DB 1 CTGCAGAGGATTAAGAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACTTTAAAGAGG 60
 QY 594 TCGGAGGTAAAGACGCAAGCCTTTCCCGAGCTGCGGAAGGCAAGTCCTTCATG 653
 DB 61 TCGGAGGTAAAGACGCAAGCCTTTCCCGAGCTGCGGAAGGCAAGTCCTTCATG 120
 QY 654 GCGGGAATGGAACCTTAATTTCCCGTTCCGCCCAACACAGCCGCCCGAGAGAGTACTC 713
 DB 121 GCGGGAATGGAACCTTAATTTCCCGTTCCGCCCAACACAGCCGCCCGAGAGAGTACTC 180
 QY 714 TCACGAGAGCCCGAGAGTCAGCTTGAGCCATCCGTGCGGTGCGCGCTTCCTTTAT 773
 DB 181 TCACGAGAGCCCGAGAGTCAGCTTGAGCCATCCGTGCGGTGCGCGCTTCCTTTAT 240
 QY 774 AACCCAGTCTGCCCGAGAGGACGCGGTTGCGGAGAGGTGGGCTCGGAGAGGTGGTGGC 833
 DB 241 AACCCAGTCTGCCCGAGAGGACGCGGTTGCGGAGAGGTGGGCTCGGAGAGGTGGTGGC 300

QY 834 CATTTTGTCTAACCCTACTGAGAGGCGGTA 867
 DB 301 CATTTTGTCTAACCCTACTGAGAGGCGGTA 334

RESULT 10
 AAT89242
 ID AAT89242 standard; DNA; 981 BP.
 XX
 AC AAT89242;
 XX
 DT 12-MAY-1998 (first entry)
 XX
 DE Clone containing htr sequence.
 XX
 KW Peptide nucleic acid; PNA; cancer; telomerase; probe; hybridisation;
 KW inhibitor; human telomerase RNA; htr; ds.
 XX
 OS Homo sapiens.
 XX
 OS Synthetic.
 OS
 FH Key Location/Qualifiers
 FT misc_difference 265..716
 FT /*tag= a
 FT /note= "human telomerase RNA"

PN WO9738013-A1.
 XX
 PD 16-OCT-1997.
 XX
 PF 09-APR-1997; 97WO-0505931.
 XX
 PR 09-APR-1996; 96US-0630019.
 XX
 PA (GERO-) GERON CORP.
 XX
 PI COREY D, NORTON JC, PIATYSZEK MA, SHAY JW, WRIGHT WE;
 XX
 DR WPI; 1997-512647/47.
 XX
 PT New peptide nucleic acids hybridising to mammalian telomerase RNA -
 PT used to inhibit telomerase, for treating tumours and other
 PT proliferative diseases, also for diagnosis
 XX
 PS Disclosure; Pages 20-21; 76pp; English.

CC This fragment of cloned DNA contains the human telomerase RNA (htr)
 CC sequence, (266-716bp). The htr region contains a CCC template which
 CC the peptide nucleic acid (PNA) can recognise. The presence of a GGG
 CC in the PNAs allows for the specific hybridisation to the template
 CC region of this htr component. PNAs can be used as probes to detect the
 CC RNA component of mammalian telomerase and as inhibitors of telomerase
 CC activity, especially in the treatment of cancer.

SO Sequence 981 BP; 172 A; 303 C; 305 G; 200 T; 1 other;

Query Match 38.3%; Score 332.4; DB 18; Length 981;
 Best Local Similarity 99.7%; Pred. No. 3.6e-96;
 Matches 333; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 534 CTGCAGAGGATTAAGAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACTTTAAAGAGG 593
 DB 1 CTGCAGAGGATTAAGAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACTTTAAAGAGG 60
 QY 594 TCGGAGGTAAAGACGCAAGCCTTTCCCGAGCTGCGGAAGGCAAGTCCTTCATG 653
 DB 61 TCGGAGGTAAAGACGCAAGCCTTTCCCGAGCTGCGGAAGGCAAGTCCTTCATG 120
 QY 654 GCGGGAATGGAACCTTAATTTCCCGTTCCGCCCAACACAGCCGCCCGAGAGAGTACTC 713
 DB 121 GCGGGAATGGAACCTTAATTTCCCGTTCCGCCCAACACAGCCGCCCGAGAGAGTACTC 180
 QY 714 TCACGAGAGCCCGAGAGTCAGCTTGAGCCATCCGTGCGGTGCGCGCTTCCTTTAT 773

Db 181 TCACGAGAGCGCGGAGGTAGCTTGCCCAATCCGTGCGCGCGCCCTCCCTTTAT 240
 QY 774 AACCCGACTGCGCGGAGCGCACACCGGTTGCGAGAGGTGGGCTGGAGAGGGTGGTGGC 833
 Db 241 AACCGACTGCGCGGAGCGCACACCGGTTGCGAGAGGTGGGCTGGAGAGGGTGGTGGC 300
 QY 834 CATTGTTTGTCTAACCTTAAGAGAGGCGCTA 867
 Db 301 CATTGTTTGTCTAACCTTAAGAGAGGCGCTA 334
 RESULT 11
 AAV63644 standard; DNA: 981 BP.
 AAV63644:
 15-FEB-1999 (first entry)
 Human telomerase RNA component sequence from lambda clone 28-1.
 Lambda clone 28-1: human; telomerase RNA component; anticancer therapy;
 assay: vaccine; cancer; purification; ss.
 OS Homo sapiens.
 OS Synthetic.
 FH Key location/Qualifiers
 FT mISC-feature 266..716
 FT /tag= "human telomerase RNA component sequence"
 PN MO9845450-A1.
 PD 15-OCT-1998.
 PF 04-APR-1997: 97WO-US06012.
 PR 04-APR-1997: 97WO-US06012.
 PA (GERO-) GERON CORP.
 PI Atkinson EM, Kealey JT, Lichtsteiner SP, Pruzan RA;
 PI Vasserot AP, Weinrich SL;
 DR WPI: 1998-594485/50.
 PT Purification of telomerase on affinity material - useful for, e.g.
 PT diagnosis and treatment of cancer
 PS Disclosure: Pages 14-15; 76pp; English.
 CC The present sequence represents the pSti fragment of the 2.4 kb
 CC Sautitai-HindIII fragment of lambda clone 28-1. This clone contains
 CC human telomerase RNA component gene sequences. The specification
 CC provides methods for purifying human telomerase. The methods involve
 CC the use of several sequential steps, including the use of two matrices
 CC that bind molecules bearing negative charges; a matrix that binds
 CC molecules bearing positive charges; an affinity purification step
 CC and a size separation. Telomerase is a particularly target of anticancer
 CC therapies, and is useful in assays for characterizing (pre)cancerous
 CC cells. The present sequence can be used for such assays. Telomerase can
 CC also be used to screen for specific modulators, for biochemical analysis
 CC of its activity, and in preparation of antibodies. Fragments of
 CC telomerase, or nucleic acid encoding them, are used in vaccines, and
 CC for treating over expression of telomerase, particularly in cancer.
 SQ Sequence 981 BP; 172 A; 303 C; 305 G; 200 T; 1 other;
 Query Match 38.3%; Score 333.4; DB 19; Length 981;
 Best Local Similarity 99.7%; Pred. No. 3,6e-96;
 Matches 333; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 534 CTCGAGAGATAGAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAG 593
 Db 1 CTCGAGAGATAGAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAG 60
 QY 594 TCGGAAGTAAAGACGCAAAAGCTTTCCGAGCTGGCGGAAGGGCAACGTCCTTCATG 653
 Db 61 TCGGAAGTAAAGACGCAAAAGCTTTCCGAGCTGGCGGAAGGGCAACGTCCTTCATG 120
 QY 654 GCCGGAATGGAACCTTAATTTCCGTTCCCGCCCAACACGACCGCCCGAGAGAGTACATC 713
 Db 121 GCCGGAATGGAACCTTAATTTCCGTTCCCGCCCAACACGACCGCCCGAGAGAGTACATC 180
 QY 714 TCACGAGAGCGCGGAGAGTACAGCTTGCCCAATCCGTGCGCGCGCCCTCTTTAT 773
 Db 181 TCACGAGAGCGCGGAGAGTACAGCTTGCCCAATCCGTGCGCGCGCCCTCTTTAT 240
 QY 774 AACCCGACTGCGCGGAGCGCACACCGGTTGCGAGAGGTGGGCTGGAGAGGGTGGTGGC 833
 Db 241 AACCCGACTGCGCGGAGCGCACACCGGTTGCGAGAGGTGGGCTGGAGAGGGTGGTGGC 300
 QY 834 CATTGTTTGTCTAACCTTAAGAGAGGCGCTA 867
 Db 301 CATTGTTTGTCTAACCTTAAGAGAGGCGCTA.334
 RESULT 12
 AA23626 standard; DNA: 981 BP.
 AA23626:
 07-JAN-2000 (first entry)
 Human clone 28-1 containing telomerase fragment.
 Telomerase; human; immune response; cancer; vaccine; treatment;
 disease; ss.
 OS Homo sapiens.
 PN US5968506-A.
 PD 19-OCT-1999.
 PF 04-APR-1997: 97US-0833377.
 PR 04-AUG-1995: 95US-0510736.
 PA (GERO-) GERON CORP.
 PI Atkinson EM, Lichtsteiner SP, Weinrich SL, Pruzan RA, Kealey JT;
 PI Vasserot AP;
 DR WPI: 1999-590379/50.
 PT Compositions comprising human telomerase, useful for treating diseases
 PT associated with overexpression of telomerase e.g. cancer -
 PS Disclosure: Column 41-42; 34pp; English.
 CC This invention describes a novel composition comprising human telomerase
 CC having at least 2000-fold (preferably at least 6000-fold) increased
 CC relative purity compared with crude extract of cells from
 CC adenovirus-transformed kidney cell line. The composition is useful for
 CC eliciting an immune response in animals and may therefore be used as a
 CC vaccine for treating diseases associated with the overexpression of
 CC telomerase e.g. cancer. This sequence represents a nucleic acid fragment
 CC from human clone 28-1 which contains a fragment of the human telomerase
 CC described in the method of the invention.
 SQ Sequence 981 BP; 172 A; 303 C; 305 G; 200 T; 1 other;


```
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FT misc_feature 266..716
FT /tag= a
FT /note= "htr gene sequence"
FT misc_feature 311..320
FT /tag= b
FT /note= "Template region of htr used as template for
FT synthesis of telomeric repeats"
XX
XX US6294650-B1.
XX
XX 25-SEP-2001.
XX
XX 08-JUL-1999: 99US-0349532.
XX
XX 09-APR-1997: 97US-0838545.
XX 09-APR-1996: 96US-0630019.
XX
XX (TEXA ) UNIV TEXAS SYSTEM.
XX
XX Shay JW, Wright WE, Platyszek MA, Corey DR, Norton JC;
XX MPI: 2001-638024/73.
XX
XX New peptide nucleic acids that hybridises to the RNA component of
XX mammalian telomerase, useful for treating or preventing cancer,
XX inflammation, lymphoproliferative diseases, autoimmune disease, or
XX neurodegenerative diseases
XX
XX Disclosure: Column 13-16; 46pp: English.
XX
XX
XX CC The present invention relates to peptide nucleic acids (PNAs), comprising
XX a sequence of 6-25 nucleobases, that inhibit telomerase activity in
XX mammalian cells by hybridising to the RNA component of mammalian
XX telomerase. The PNAs are useful as probes to detect the RNA component
XX of mammalian telomerase and as inhibitors of telomerase activity, or to
XX detect and/or quantitate polynucleotide having the human telomerase
XX RNA component (htr) sequence, as well as in forensic identification of
XX individuals, such as paternity testing or identification of criminal
XX suspects or unknown descendants based on the htr gene RFLP pattern. The
XX PNA can be further used for treating or preventing cancer, inflammation,
XX lymphoproliferative diseases, autoimmune disease, or neurodegenerative
XX diseases. The PNAs in combination with other pharmaceuticals (such as
XX antineoplastic or cytostatic agents) can be used for treating neoplasia,
XX hyperplasia, human immunodeficiency virus (HIV) infections, acquired
XX immunodeficiency syndrome (AIDS) and associated pathologies, and other
XX diseases characterised by abnormal telomere metabolism or telomerase
XX activity. The present sequence represents a PstI fragment, derived
XX from bacteriophage lambda clone 28-1, containing the htr gene sequence.
XX
XX Sequence 981 BP; 172 A; 303 C; 305 G; 200 T; 1 other:
XX
XX Query Match 38.3%; Score 332.4; DB 23; Length 981;
XX Best Local Similarity 99.7%; Pred. No. 3,6e-96;
XX Matches 333; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 534 CTCACAGAGTAAAGAAAAGCCCTCTGATACCTCAAGTTAGTTTACCTTTAAAGAG 533
XX 1 CTCACAGAGTAAAGAAAAGCCCTCTGATACCTCAAGTTAGTTTACCTTTAAAGAG 60
XX
XX QY 594 TCGGAAGTAAGACCAAGCCTTTCCCGAGCTGCGGAAGGCAAGCTCTTCCATG 653
XX TCGGAAGTAAGACCAAGCCTTTCCCGAGCTGCGGAAGGCAAGCTCTTCCATG 120
XX
XX QY 654 GCCGGAATGAACTTAAATTTCCCGTCCCAACCAAGCCCGCCGAGAGTGAATC 713
XX GCCGGAATGAACTTAAATTTCCCGTCCCAACCAAGCCCGCCGAGAGTGAATC 180
XX
XX QY 714 TCACGAGAGCCCGGAGAGTACCTTGCGCAATCCGTGCGGCGCCCTCCCTTAT 773
XX TCACGAGAGCCCGGAGAGTACCTTGCGCAATCCGTGCGGCGCCCTCCCTTAT 240
XX
XX Db 181 TCACGAGAGCCCGGAGAGTACCTTGCGCAATCCGTGCGGCGCCCTCCCTTAT 240
```

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QY 774 AACCCACTCGCCCGCAGCCACCCGGTTGCGAGAGTGGCCCTGGAGGCGTGTGCG 833
XX
XX Db 241 AACCCACTCGCCCGCAGCCACCCGGTTGCGAGAGTGGCCCTGGAGGCGTGTGCG 300
XX
XX QY 834 CATTTTGTCTAACCTTAACCTGAGAGAGGCGTA 867
XX CATTTTGTCTAACCTTAACCTGAGAGAGGCGTA 334
XX
XX Db 301 CATTTTGTCTAACCTTAACCTGAGAGAGGCGTA 334
XX
XX RESULT 15
XX AAZ07323
XX ID AAZ07323 standard; DNA; 176 BP.
XX
XX AC AAZ07323:
XX
XX DT 22-OCT-1999 (first entry)
XX
XX DE Human telomerase RNA (htr) proximal promoter (nucleotides -107 to +69).
XX
XX KM Telomerase RNA; TR: promoter; cytotoxin; cancer; neoplasia; htr:
XX gene therapy; thymidine kinase gene; anticancer therapy; human; ss.
XX
XX OS Homo sapiens.
XX
XX PN MO9938964-A2.
XX
XX PD 05-AUG-1999.
XX
XX PF 29-JAN-1999: 99WO-GB00308.
XX PR 29-JAN-1998: 98GB-0001902.
XX
XX (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
XX
XX Keith WN;
XX MPI: 1999-479183/40.
XX
XX PT Mouse and human telomerase RNA gene promoters, useful for tumor
XX specific gene therapy
XX
XX Disclosure: Fig 19; 109pp: English.
XX
XX CC The invention relates to promoter regions from mouse and human telomerase
XX RNA (TR) component genes. The TR gene promoter can be linked to a
XX heterologous gene, especially a gene encoding a cytotoxin, for therapy
XX of cancer, especially neoplasias. The telomerase is necessary for the
XX unrestricted proliferative capacity of many human cancers. Mutation or
XX dysregulation of the telomerase repression pathway may cause reactivation
XX or upregulation of telomerase expression in cancer. Substances
XX identified in the methods, can be used to block transcription from the TR
XX gene promoter through interaction of the 5' regulatory sequences. These
XX substances, e.g. antisense oligonucleotides, transcription factors,
XX peptide nucleic acids and factors that disrupt signal transduction, are
XX useful for cancer therapy. In particular, gene therapy vectors
XX (especially pGR62-codAup) comprising the promoter and a viral thymidine
XX kinase gene can be used to convert a prodrug, e.g. gancyclovir, so that
XX neoplasia can be controlled or treated. Direct down-regulation of
XX telomerase RNA gene through manipulation of transcription factors may be
XX effective anticancer therapy and the cloning of the htr gene promoter
XX allows the analysis of therapeutic molecules which modulate htr promoter
XX activity. The present sequence represents a human TR gene (htr)
XX proximal promoter region.
XX
XX SQ Sequence 176 BP; 30 A; 51 C; 63 G; 32 T; 0 other:
XX
XX Query Match 20.3%; Score 176; DB 20; Length 176;
XX Best Local Similarity 100.0%; Pred. No. 2,8e-46;
XX Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 692 AGCCGCGCGAGAGTACTCTACAGAGAGCCGCGAGAGTCAAGTTGCGCAATCCGTGC 751
XX
XX
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Db 1 AGCCCGCCGAGAGAGTCACTCTACGAGAGCCGCGAGAGTCACTTGCCAAATCCGTGC 60
QY 752 GGTGGGGGGCGGCTCCCTTTATAAGCCGACTCGCCGCGCAGCGACCGGGSTGCGGAGGG 81.1
Db 61 GGTGGGGGGCGGCTCCCTTTATAAGCCGACTCGCCGCGCAGCGACCGGGSTGCGGAGGG 120
QY 812 TGGGCTTGGGAGGGGTGTGCGCCATTTTGTCTAACCTTAAGAGAGGGCGTA 867
Db 121 TGGGCTTGGGAGGGGTGTGCGCCATTTTGTCTAACCTTAAGAGAGGGCGTA 176

Search completed: January 25, 2003, 14:59:34
job time : 315 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 25, 2003, 13:41:20 : Search time 92 Seconds
(without alignments)
4233.833 Million cell updates/sec

Title: US-09-601-267-36
Perfect score: 867
Sequence: 1 agctactcaggagcgtcgtaga.....ccctactcaggagcgtcgtaga 867

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 396772 seqs, 224632407 residues

Total number of hits satisfying chosen parameters: 793544

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*

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- 2: /cgn2_6/ptodata/2/pubpna/PCOT_NEW_PUB.seq:*
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- 11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	848.6	97.9	2426	10 US-09-057-351-3	Sequence 3, Appl1
2	109.2	12.6	133893	9 US-10-161-510-1	Sequence 1, Appl1
3	101.8	11.7	180216	10 US-09-835-232-6	Sequence 6, Appl1
4	101.2	11.7	32193	10 US-09-764-877-2623	Sequence 2623, Ap
5	101.2	11.7	684973	10 US-09-263-959-1	Sequence 1, Appl1
6	99.6	11.5	302250	10 US-09-962-832-154	Sequence 154, Ap
7	99.2	11.4	9914	10 US-09-764-847-1558	Sequence 1558, Ap
8	99	11.4	31994	9 US-09-764-904-71	Sequence 71, Appl1
9	99	11.4	31994	10 US-09-764-860-599	Sequence 599, Ap
10	98.6	11.4	28897	10 US-09-764-877-3897	Sequence 3897, Ap
11	98	11.3	289	10 US-09-764-877-2732	Sequence 2732, Ap
12	97.6	11.3	2756	10 US-09-764-853-898	Sequence 898, Ap
13	97.4	11.2	27148	10 US-09-764-860-1046	Sequence 1046, Ap
14	97	11.2	10885	10 US-09-764-877-3843	Sequence 3843, Ap
15	96.4	11.1	30625	10 US-09-927-091-5	Sequence 5, Appl1
16	96.4	11.1	32187	10 US-09-764-847-1550	Sequence 1550, Ap
17	96.4	11.1	32193	10 US-09-764-847-1549	Sequence 1549, Ap
18	96.4	11.1	145831	10 US-09-963-708-79	Sequence 79, Appl1
19	96.4	11.1	145831	10 US-09-954-456-2116	Sequence 2116, Ap

C 20	96	11.1	303	10 US-09-764-870-604	Sequence 604, Ap
C 21	96	11.1	1115	9 US-09-981-353-126	Sequence 126, Ap
C 22	96	11.1	1545	10 US-09-764-877-3172	Sequence 3172, Ap
C 23	96	11.1	10378	10 US-09-764-847-1616	Sequence 1616, Ap
C 24	96	11.1	10472	10 US-09-764-847-1615	Sequence 1615, Ap
C 25	96	11.1	17752	10 US-09-748-127-3	Sequence 3, Appl1
C 26	96	11.1	32193	10 US-09-764-877-3171	Sequence 3171, Ap
C 27	96	11.1	32193	9 US-09-764-868-1508	Sequence 1508, Ap
C 28	96	11.1	53542	10 US-09-801-574-61	Sequence 61, Appl1
C 29	96	11.1	98865	10 US-09-770-669A-3	Sequence 3, Appl1
C 30	95.8	11.0	2240	10 US-09-814-282-1	Sequence 1, Appl1
C 31	95.6	11.0	423	10 US-09-867-701-7043	Sequence 7043, Ap
C 32	95.4	11.0	36159	12 US-10-135-687-3	Sequence 3, Appl1
C 33	95	11.0	32169	10 US-09-764-887-1963	Sequence 1963, Ap
C 34	95	11.0	32190	10 US-09-764-887-3389	Sequence 3389, Ap
C 35	94.8	10.9	142	10 US-09-764-877-3289	Sequence 3289, Ap
C 36	94.8	10.9	4071	10 US-09-764-869-2040	Sequence 2040, Ap
C 37	94.8	10.9	32195	10 US-09-764-870-611	Sequence 611, Ap
C 38	94.8	10.9	32195	10 US-09-764-870-617	Sequence 617, Ap
C 39	94.8	10.9	32195	10 US-09-764-869-1605	Sequence 1605, Ap
C 40	94.8	10.9	176373	9 US-10-095-407-17	Sequence 17, Appl1
C 41	94.6	10.9	7017	10 US-09-764-877-3773	Sequence 3773, Ap
C 42	94.6	10.9	8868	10 US-09-803-670-3	Sequence 3, Appl1
C 43	94.6	10.9	20522	10 US-09-764-877-3774	Sequence 3774, Ap
C 44	94.6	10.9	21470	10 US-09-764-847-1157	Sequence 1157, Ap
C 45	94.4	10.9	311	9 US-09-860-670-199	Sequence 199, Ap

ALIGNMENTS

RESULT 1
US-09-057-351-3
Sequence 3, Application US/09057351
Patent No. US20010034439A1
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/057,351
FILING DATE: 08-APR-1994
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/472,802
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-000821US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2426 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-057-351-3

Query Match 97.9% Score 848.6; DB 10; Length 2426;
Best Local Similarity 99.4%; Pred. No. 1.1e-242;
Matches 862; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

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Db 662 ACCTACTCAGAGGCTGACACAGACGATCGCTTGAACCCGGAGGACAGGTTGAGTG 720
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Db 721 AGCCGAGATCAGGCCACTGATCCATCCAGCCCTGGGCGAAGAGCAAGCTCCGTCTCA 780
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Db 781 AAAAAAAAAATGTTACATTTATGTTGATTTACTCCCTCTTTTACCTCATCAAGACA 840
181 CAGCACTACTTTAAAGCAAGTCATGATTTGAAGCGCTTTCTTCTAATAAAGGAG 240
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241 ATTCACTCTTAAGATTAATTAATGATTAACCTTGAATTAAGCCATCCCTCTCTCA 300
Db 901 ATTCACTCTTAAGATTAATTAATGATTAACCTTGAATTAAGCCATCCCTCTCTCA 960
301 AGAGAAAGTGGAGAGGATCTTAAGAGAAAAAGGGGCGAGGTGCACTCGAGCCATC 360
Db 361 AGAGAAAGTGGAGAGGATCTTAAGAGAAAAAGGGGCGAGGTGCACTCGAGCCATC 420
421 CCAGTGAAGCGGAGACAAAGTTCGCTGATGTCGCTGCGTGGGAATCTATTTCACAA 480
Db 481 CCAGTGAAGCGGAGACAAAGTTCGCTGATGTCGCTGCGTGGGAATCTATTTCACAA 1080
1081 AGTTCTCAAAAAATGTGATCAAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1140
1141 AAATCTCTCTGATTTTCAATTTTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1200
1201 GATAGAAAAAGGCGCTCTGATCAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1260
1261 TAAAGAGCAAAAGCCTTCCGAGAGTGGGCAAGGCAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1320
1321 ATGGAACCTTTATTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCT 1380
1381 ATGGAACCTTTATTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCT 1440
1441 ATGGAACCTTTATTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCT 1500
1501 ATGGAACCTTTATTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCT 1560

RESULT 2
US-10-161-510-1/c
; Sequence 1, Application US/10161510
; Publication No. US20020192695A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: PIRAS AS MODIFIERS OF THE P53 PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX02-074C
; CURRENT APPLICATION NUMBER: US/10/161,510
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US 60/296,076
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/328,605
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/357,253
; PRIOR FILING DATE: 2002-02-15
; SOFTWARE: Patent version 3.1
; SEQ ID NO 1
; LENGTH: 133893
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-161-510-1

Query Match 12.6% Score 109.2; DB 9; Length 133893;
Best Local Similarity 90.0%; Pred. No. 1.3e-21;
Matches 117; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

1 AGCTACTCAGAGGCTGACACAGACGATCGCTTGAACCCGGAGGACAGGTTGAGTG 60
Db 63711 AGCTACTCAGAGGCTGACACAGACGATCGCTTGAACCCGGAGGACAGGTTGAGTG 63652
61 AGCCGAGATCAGGCCACTGATCCATCCAGCCCTGGGCGAAGAGCAAGCTCCGTCTCA 120
Db 63651 AGCCGAGATCAGGCCACTGATCCATCCAGCCCTGGGCGAAGAGCAAGCTCCGTCTCA 63592
121 AAAAAAAAAA 130
Db 63591 AAAAAAAAAA 63582

RESULT 3
US-09-835-232-6/c
; Sequence 6, Application US/09835232
; Patent No. US20020096489A1
; GENERAL INFORMATION:
; APPLICANT: Leder, Philip
; APPLICANT: Leder, Benjamin
; TITLE OF INVENTION: FORMIN-2 NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 00363/052002
; CURRENT APPLICATION NUMBER: US/09/835,232
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: US 60/196,811
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 180216
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(180216)
; OTHER INFORMATION: n = A,T,C or G
US-09-835-232-6

Query Match 11.7% Score 101.8; DB 10; Length 180216;
Best Local Similarity 88.5%; Pred. No. 2.5e-19;
Matches 123; Conservative 0; Mismatches 12; Indels 4; Gaps 1;

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QY      1  AGCTACTCAGAGGCTGAGACAGAGAAATCGCTTGAACCCGGGAGGCAGAGTTGCAGTG 60
          |||
Db 64485  AGCTACTCAGAGGCTGAGACAGAGAAATGCTTGAACCCGGGAGGCAGAGTTGCAGTG 64426
QY      61  AGCCGAGATCAGCCCACTAGATCCATCCAGCCTGGGCGAAGAGCAAGACTCCGCTCTCA 120
          |||
Db 64425  AGCCGAGATCAGCCCACTAGATCCATCCAGCCTGGGCGAAGAGCAAGACTCCGCTCTCA 64370
QY      121  AAAAAAAAAAAGTGTATTA 64351
          |||
Db 64369  AAAAAAAAAAAGTGTATTA 64351

RESULT 4
US-09-764-877-2623/c
; Sequence 2623, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2623
; LENGTH: 32193
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-2623

Query Match
Best Local Similarity 11.7%; Score 101.2; DB 10; Length 32193;
Matches 112; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY      1  AGCTACTCAGAGGCTGAGACAGAGAAATCGCTTGAACCCGGGAGGCAGAGTTGCAGTG 60
          |||
Db 31984  AGCTACTCAGAGGCTGAGAGGAGAGAAATGCTTGAACCCGAGAGGAGGTTAGCAATG 31925
QY      61  AGCCGAGATCAGCCCACTAGATCCATCCAGCCTGGGCGAAGAGCAAGACTCCGCTCTCA 120
          |||
Db 31924  AGCTGAGATCGTGCACACTGCATCTCCAGCCTGGGCAACAGAGTAAGACTCTATCTCA 31865
QY      121  AAAAAAAAAA 130
          |||
Db 31864  AAAAAAAAAA 31855

RESULT 5
US-09-263-959-1/c
; Sequence 1, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Rowen, Lee
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTIL
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,959
```

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; FILING DATE: 05-MAR-1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 920010.426C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 684973 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-263-959-1

Query Match
Best Local Similarity 11.7%; Score 101.2; DB 10; Length 684973;
Matches 112; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY      1  AGCTACTCAGAGGCTGAGACAGAGAAATCGCTTGAACCCGGGAGGCAGAGTTGCAGTG 60
          |||
Db 442801  AGCTACTCAGAGGCTGAGAGGAGAGATGCGCTAAACCCGGGAGGCAGAGTTGCAGTG 442742
QY      61  AGCCGAGATCAGCCCACTAGATCCATCCAGCCTGGGCGAAGAGCAAGACTCCGCTCTCA 120
          |||
Db 442741  AGCCGAGATCGTGCACACTGCATCTCCAGCCTGGGAGAGACAGACACTCTGTCTCA 442682
QY      121  AAAAAAAAAA 130
          |||
Db 442681  AAAAAAAAAA 442672

RESULT 6
US-09-962-832-154/c
; Sequence 154, Application US/09962832
; Patent No. US20020110821A1
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Sign
; FILE REFERENCE: 689290-74
; CURRENT APPLICATION NUMBER: US/09/962,832
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/60/235,077
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,280
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 154
; LENGTH: 302250
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-962-832-154

Query Match
Best Local Similarity 11.5%; Score 99.6; DB 10; Length 302250;
Matches 111; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY      1  AGCTACTCAGAGGCTGAGACAGAGAAATCGCTTGAACCCGGGAGGCAGAGTTGCAGTG 60
          |||
Db 226482  AGCTACTCAGAGGCTGAGAGGAGAGAAATGCTTGAACCCGGGAGGCAGAGTTGCAGTG 226423
QY      61  AGCCGAGATCAGCCCACTAGATCCATCCAGCCTGGGCGAAGAGCAAGACTCCGCTCTCA 120
          |||
Db 226422  AGCCGAGATCAGCACTAGATCCATCCAGCCTGGGCGAAGAGCAAGACTCCATCTCA 226363
QY      121  AAAAAAAAAA 130
          |||
Db 226362  AAAAAAAAAA 226353
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	Query Match	Similarity	11.4%	Score 99.2	DB 10	Length 9914	
	Best Local	Similarity	78.2%	Pred. No. 3.2e-19			
	Matches 133	Conservative	0	Mismatches 33	Indels 4	Gaps 1	
Qy	1	AGCTACTCAGCAGCGCTGAGACACAGAAATCCGTTGACCCGGAGAGCAGGTTGCAGTG	60				
Db	8437	AGCTACTCAGAGAGCGCTGAGCGAGGAGAAATCGCTTGAACTGGGAGGACGAGTTGCAGTG	8378				
Qy	61	AGCCGAGATCACGCCACTGAGACTCCATCCAGCCTGGGCGAAGAGCAGACGTCGCTCTCA	120				
Db	8377	AGCCAGAGATTGGCGACAGTCGCACTC----CAGCTGGGTGACAGAGCAGACGACTGCTCTCA	8322				
Qy	121	AAAAAAAAAATCGTTACATTTATGTGGATTACTCCCTCTTTTACT	170				
Db	8321	AAAAAAAAAATGTTTCTTTTCTTTTAAATATAGCCAGGCTGGTGCGAT	8272				

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RESULT 8
US-09-764-904-71/c
; Sequence 71, Application US/09764904
; Patent No. US2002017345A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA122
; CURRENT APPLICATION NUMBER: US/09/764,904
; PRIORITY FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 71
; LENGTH: 31994
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-904-71

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Query Match Similarity	11.4%	Score 99:	DB 9:	length 31994;
Best Local Similarity	82.0%	Pred No.	6.8e-19:	
Matches 114; Conservative	0;	Mismatches	25;	Indels 0; Gaps 0
QY	1	AGCTACTCAGGAGGGCTGTGACACGAGAAATCGGTTGAACCCGGGAGCGACAGGTTGCGATG	60	
Db	5801	AGTTACTGTTGGAGGGCTGTGAGACAGGAAATCGGTTGAACTCGGGAGGTGAGGTTCAGAG	5742	
QY	61	AGCGGAGATCACGCCACTGTAGACTCCATCCAGCCTTGCGGCGAAGGAGCAAGATCCGTCTCA	120	
Db	5741	AGCCGAGATGCGACCACTTGTCCACCCGAGCGCTGGGCAACAGACAAAGCAACTATGTCTCA	5682	
QY	121	AAAAAAAAAATCGTTACAA	139	
Db	5681	AAAAACAAAAACAAAAACAA	5663	

Query Match	11.4%	Score 99	DB 10	Length 31994
Best Local Similarity	82.0%	Pred. No. 6,8e-19		
Matches 114	Conservative 0	Mismatches 25	Indels 0	Gaps 0
QY	1	AGCTACTCAGGAGGCTGAGACACGAGAAATCGCTTGAACCCGGGAGGACGAGGTTGCAGTG	60	
Db	5801	AGTTACTTGCGAGGCTGAGACAGGAGAAATCGCTTGAACCTGGGAGGTTGCAGTG	5742	
QY	61	AGCCGAGATCAGCCACTGACTCCATCCAGCCTGGGCGCAAAAGACAGACTTCCTGTCA	120	
Db	5741	AGCCGAGATGCGACCATGTGCACCCGACGCGCTGGGCAACAGACAGACTATGTCTCA	5682	
QY	121	AAAAAAAAAATCGTTACAA	139	
Db	5681	AAAAACAAAACAAAAACA	5663	

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RESULT 10
US-09-764-877-3897/C
; Sequence 3897, Application US/09764877
; Patent No. US0020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3897
; LENGTH: 28897
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-3897

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Query	Match	Similarity	Score	DB	Length
Best Local	169	Conservative	0	Mismatches	94; Indels 4; Gaps 1
Qy	1	ACTACTCAGAGAGCTGAGACACAGAAATCCCTTGAACCCGGGAGGACGAGGTTCAGTG	60		
Db	9456	ACTCTCTTGAGAGCTGAGACGAGGAATGGGTGAACCTGGGAGGCGAGCTTGACAGTG	9397		
Qy	61	AGCCGAGATCAGCGCACTAGACTCCATCCAGCTGGCGGCAAAAGACAAAGCTCCGTCTCA	120		
Db	9396	AGCCGAGATCCCGCACTGCAC-----TCCAGCGCTGGGCGACAGAGCAAGTCCGCTCA	9341		
Qy	121	AAAAAAAAAATCGTTAGCAATTATGGTGAATACGCCCTCTTTTAACTCATCAAGACA	180		
Db	9340	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAACACCTGATTACTTTTAATTAAGT	9281		
Qy	181	CAGCACTACTTTAAAGCAAGTCAATGATGGAAGCGCTTTTCTTCTTAATTAAGGAG	240		

Query Match	11.2%	Score 97;	DB 10;	Length 10885;
Best Local Similarity	82.1%;	Pred. NO. 1.5e-18;		
Matches 124; Conservative	0;	Mismatches 25;	Indels 2;	Gaps 1;

QY 1 AGCTACTCAGGAGGCTGAGACACCGAATGCTTGAACCCGGGAGCGACAGAGGTTCAGTG 60
|||||
Db 6432 AGCTACTCTGAGGCTGAGGACGAGAAATGCTTGAACCCGGGAGCGACAGAGGTTCAGTG 6491

Qy 61 AGCCGAGTCACGCCCATCTAGACTCCTCATCCAGCCCTGGGGCAAGAAGACAAGACTCCGTCTCA 120
 ||||| ||||| ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 6492 AGCCGGGATCGCACACCACCTCTGCAC--TCCAACCTGGGTGACAGAGACAAGACTCCGTCTCA 6549

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QY 121 AAAAAAAAAATCGTTACAAITTTATGCTGCAT 151
      |||||
Db 6550 AAAAAAAAAAAAAAAAAAACCGTAGTT 6580

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RESULT 15
US-09-927

US-09-927-091-5

Sequence 5, Application US/09927091

Patent No. US20020119541A1

APPLICANT: KILLABY

APPLICANT: IOTT, STEVE

APPLICANT: CHANDLER, DAWN

1; TITLE OF INVENTION: THE TUMOR SUPPRESSOR CAR-1

FILE REFERENCE: UTSC:651US

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CURRENT FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 60/0327 440

PRIOR FILING DATE: 2000-08-23

PRIOR APPLICATION NUMBER: 60/225.033

PRIOR FILING DATE: 2000-08-10

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 5

LENGTH: 30625
TYPE: DNA

ORGANISM: HUM

FEATURE:

NAME/KEY: mod

; LOCATION: (4754

OTHER INFORMATION: n =

US-09-927-091-5

11 Question Match

query malc11	11.18;	score 96.4;
Best local similarity	83.88;	Prod No 4

Matches 109:

[illegible]

6859 AGCCATTCAAGAGGCTGGCGCAGAGAATTCCTTGACCTGGAGGCCAAGGTTCACAGT 691B

D6 6919 AGCCAGATCTCACACCATGCACTTCATTCCAGCCTGGGTGACAGAGACAAGACTCTAACTTA 6978

QY	121	AAAAAAA	130
Db	6979	AAAAAAAAA	6986

Search completed: January 25, 2003, 15:05:47
Job time : 794 secs